

# Sequence Listing

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 Hillan, Kenneth J  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
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 Shelton, David L.  
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 Tumas, Daniel  
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 Wood, William I.

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 <212> PRT  
 <213> Homo sapiens

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                   20                  25                  30  
 Glu Gln Ala Leu Asn Arg Gly Ile Ala Ala Val Lys Glu Asp Ala  
                   35                  40                  45  
 Val Glu Met Leu Ala Ser Tyr Gly Leu Ala Tyr Ser Leu Met Lys

50										55					60				
Phe	Phe	Thr	Gly	Pro	Met	Ser	Asp	Phe	Lys	Asn	Val	Gly	Leu	Val					
				65					70					75					
Phe	Val	Asn	Ser	Lys	Arg	Asp	Arg	Thr	Lys	Ala	Val	Leu	Cys	Met					
				80					85					90					
Val	Val	Ala	Gly	Ala	Ile	Ala	Ala	Val	Phe	His	Thr	Leu	Ile	Ala					
				95					100					105					
Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val					
				110					115					120					
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu					
				125					130					135					
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly					
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Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser					
				155					160					165					
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu					
				170					175					180					
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu					
				185					190					195					
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
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Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
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Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
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Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val Asp
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Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe Ser
	365	370 375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly Trp
	380	385 390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser Val
	395	400 405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro Tyr
	410	415 420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu Ala
	425	430 435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys Tyr
	440	445 450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala Thr
	455	460 465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu Glu
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Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu
	485	490

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<220>  
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 <222> 33, 66, 96, 387  
 <223> unknown base

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 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
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 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
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<210> 13  
<211> 18  
<212> DNA  
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<220>  
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<400> 13  
tcattctcttc cctctccc 18

<210> 14  
<211> 18  
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<400> 14  
ccttccgccg cggagttc 18

<210> 15  
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<210> 16  
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<212> DNA  
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<400> 16  
gcctgctgtg gtcacaggtc tccg 24

<210> 17  
<211> 45  
<212> DNA  
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<220>  
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<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
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<212> DNA  
<213> Homo sapiens

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ccgtgagccg cctcatcttc acgttcttcc tcttctctggg ggtgctggtg 200  
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gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400  
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FOOTNOT 66292660



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a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro
				20					25					30
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe
				35					40					45
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly
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09078299-101504

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
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Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

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Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu	
365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr	
380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met	
395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met	
410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp	
425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu	
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<210> 20  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 20  
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<210> 21  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 21  
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<210> 22  
 <211> 20  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 22  
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<210> 23  
 <211> 18

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcacc acgg 24

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggctcagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
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<210> 28  
<211> 285  
<212> PRT  
<213> Homo sapiens

<400> 28  
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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
20 25 30

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Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

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 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
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<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 262, 330, 371  
 <223> unknown base

<400> 30  
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 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
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<210> 31  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 32  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 32  
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<210> 33  
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<213> Artificial Sequence

<220>  
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<400> 33  
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<210> 34  
<211> 40  
<212> DNA  
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<210> 35  
<211> 1819  
<212> DNA  
<213> Homo sapiens

<400> 35  
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cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750  
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 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
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 taaaagaaag taatggaag 1819

<210> 36  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
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 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile  
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Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
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<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
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 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

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<210> 38
<211> 566
<212> DNA
<213> Homo sapiens
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ttacaccaat gtattctaga atagtatatgt cttaggaaaat tgtgggttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcataatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500
ggaggaaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566
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<220>  
<221> unsure  
<222> 84-85, 206  
<223> unknown base
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tggtngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 40  
accacagtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
ggcccaaaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
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tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

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gacgctgcag tgtgaggagac ctgtctgcac tgaggagagc agctgccaca 150  
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 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
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 gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400  
 cgtggtacaa aaggcagaca gggggcacta ccactgcagt ggcatcttcc 450  
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 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
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 cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtg 1200  
 tttgttagaa taatgtagt aggtgagtgt aaataaattt atataaagt 1250  
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
 totgtgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350  
 tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg 1400  
 ggggcaattt tgccccccag aggcattgg gcaatgtttg gagacatttt 1450  
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500  
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ggcagtaccc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600  
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 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000  
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<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
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 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150

09978299 "101501"

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Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala
				170					175					180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys
				185					190					195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr
				200					205					210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe
				215					220					225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys
				230					235					240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln
				245					250					255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro
				260					265					270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala
				275					280					285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser
				290					295					300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro
				305					310					315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp
				320					325					330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu
				335					340					345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
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<210> 46  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 46  
 tgggctgtgt cctcatgg 18  
  
 <210> 47  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 47  
tttccagcgc caattctc 18

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
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gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaca gtggacactt atggcgcgtc catcctggaa gtgccagaga 200  
gtgtaacagg accttggaag ggggatgtga atcttcctg cacctatgac 250  
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agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400  
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 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
 caggaaagag cctgcctgtc tttgccatca tcctcatcat ctcttgtgc 1000  
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 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
 aggtcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
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 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
 110 115 120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180

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Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr	
				185					190					195	
Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	
				200					205					210	
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	
				215					220					225	
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
				230					235					240	
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
				245					250					255	
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	
				260					265					270	
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	
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Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	
				290					295					300	
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	
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Val	Tyr	Glu	Ala	Ala	Arg										
				320											

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55  
cttcacaatg tcgctgtgct gctc 24

<210> 56  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
agccaaatcc agcagctggc ttac 24

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
tgatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58  
<211> 2458  
<212> DNA  
<213> Homo sapiens

<400> 58  
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ccagctcgcc cgaggtccgt cggagggcgc cgcccgcccc ggagccaagc 150  
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Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
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<210> 61  
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<400> 61  
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<210> 62  
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<210> 63  
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 <212> PRT  
 <213> Homo sapiens

<400> 64  
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Lys Ala Ser Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala  
50 55 60

Thr Gly Gln Val Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr  
65 70 75

Val Ser Glu His Cys Thr Asn Thr Ser Leu Arg Val Cys Ser Ser  
80 85 90

Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn Gly Ile Glu Lys  
95 100 105

Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met Ile Glu Lys  
110 115 120

Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys Pro Pro  
125 130 135

Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His Thr Val Cys  
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Pro Val Gly Trp Gly Val Arg Lys Lys Gly Thr Glu Thr Glu Asp  
155 160 165

Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val Pro  
170 175 180

Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln  
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Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val  
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Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro  
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Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
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Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu  
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Ser Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile  
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275 280 285

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His  
290 295 300

Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser  
305 310 315

Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly

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335	340	345
Ile Asn Glu His Leu	Pro Trp Met Ile Val Leu Phe Leu Leu Leu	
350	355	360
Val Leu Val Val Ile	Val Val Cys Ser Ile Arg Lys Ser Ser Arg	
365	370	375
Thr Leu Lys Lys Gly	Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	
380	385	390
Lys Ala Gly Leu Lys	Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	
395	400	405
Lys Trp Ile Tyr Tyr	Cys Asn Gly His Gly Ile Asp Ile Leu Lys	
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Phe Leu Cys Asn Ala	Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	
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Gly Tyr Thr Ala Asp	His Glu Arg Ala Tyr Ala Ala Leu Gln His	
455	460	465
Trp Thr Ile Arg Gly	Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	
470	475	480
Ala Leu Arg Gln His	Arg Arg Asn Asp Val Val Glu Lys Ile Arg	
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Gly Leu Met Glu Asp	Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	
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Leu Pro Met Ser Pro	Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	
515	520	525
Pro Asn Ala Lys Leu	Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	
530	535	540
Ser Pro Gln Asp Lys	Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	
545	550	555
Pro Leu Leu Arg Cys	Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	
560	565	570
Ser Arg Asn Gly Ser	Phe Ile Thr Lys Glu Lys Lys Asp Thr Val	
575	580	585
Leu Arg Gln Val Arg	Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe	
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Asp Asp Met Leu His	Phe Leu Asn Pro Glu Glu Leu Arg Val Ile	
605	610	615

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

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<400> 67

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<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
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 65 70 75  
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
 80 85 90  
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Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe 155 160 165		
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys 170 175 180		
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala 185 190 195		
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg 200 205 210		
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu 215 220 225		
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His 230 235 240		
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala 245 250 255		
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile 260 265 270		
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His 275 280 285		
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Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu 320 325 330		
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala 335 340 345		
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala 350 355 360		
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr 365 370 375		
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr 380 385 390		
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val 395 400 405		



Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
410 415 420

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Leu Lys Thr

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<400> 70  
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<400> 71  
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<210> 73  
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<212> DNA  
<213> Homo sapiens

<400> 73  
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gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150  
gtcagcggc ggcgcgggcg ctgcgcgagg gctccggagc tgactcgccg 200

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TDSIT 65282660

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 <212> PRT  
 <213> Homo sapiens

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 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala  
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 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
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 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
                   65                  70                  75  
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
                   80                  85                  90  
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp  
                   95                  100                  105  
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
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 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys  
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 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val  
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 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro  
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 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His  
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 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser  
                   185                  190                  195  
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr  
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Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe	Gln
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Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile	Glu
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Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile	Arg
245		250	255
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260		265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu	Asp
275		280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn	Ala
290		295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly	Met
305		310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly	Ile
320		325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr	Leu
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Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr	Leu
350		355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly	Cys
365		370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe	Ser
380		385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly	Met
395		400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe	Gly
410		415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu	Cys
425		430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn	Ala
440		445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly	Leu
455		460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys	Arg
470		475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly	Ala
485		490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His	Ser

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Cys	Gln	Asp	Val	Asp	Gly	Tyr	Cys	Tyr	Asn	Gly	Ile	Cys	Gln	Thr
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His	Glu	Gln	Gln	Cys	Val	Thr	Leu	Trp	Gly	Pro	Gly	Ala	Lys	Pro
				530					535					540
Ala	Pro	Gly	Ile	Cys	Phe	Glu	Arg	Val	Asn	Ser	Ala	Gly	Asp	Pro
				545					550					555
Tyr	Gly	Asn	Cys	Gly	Lys	Val	Ser	Lys	Ser	Ser	Phe	Ala	Lys	Cys
				560					565					570
Glu	Met	Arg	Asp	Ala	Lys	Cys	Gly	Lys	Ile	Gln	Cys	Gln	Gly	Gly
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Ala	Ser	Arg	Pro	Val	Ile	Gly	Thr	Asn	Ala	Val	Ser	Ile	Glu	Thr
				590					595					600
Asn	Ile	Pro	Leu	Gln	Gln	Gly	Gly	Arg	Ile	Leu	Cys	Arg	Gly	Thr
				605					610					615
His	Val	Tyr	Leu	Gly	Asp	Asp	Met	Pro	Asp	Pro	Gly	Leu	Val	Leu
				620					625					630
Ala	Gly	Thr	Lys	Cys	Ala	Asp	Gly	Lys	Ile	Cys	Leu	Asn	Arg	Gln
				635					640					645
Cys	Gln	Asn	Ile	Ser	Val	Phe	Gly	Val	His	Glu	Cys	Ala	Met	Gln
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Cys	His	Gly	Arg	Gly	Val	Cys	Asn	Asn	Arg	Lys	Asn	Cys	His	Cys
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Glu	Ala	His	Trp	Ala	Pro	Pro	Phe	Cys	Asp	Lys	Phe	Gly	Phe	Gly
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Gly	Ser	Thr	Asp	Ser	Gly	Pro	Ile	Arg	Gln	Ala	Glu	Ala	Arg	Gln
				695					700					705
Glu	Ala	Ala	Glu	Ser	Asn	Arg	Glu	Arg	Gly	Gln	Gly	Gln	Glu	Pro
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 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
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<210> 79  
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<210> 83  
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<210> 84  
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<400> 84  
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 <213> Homo sapiens

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 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
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<210> 88  
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<211> 2956

<212> DNA

<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45  
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
 110 115 120  
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
 125 130 135  
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
 140 145 150  
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
 155 160 165  
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
 170 175 180

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 TOSTOT 66282660

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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ccaagccaac acactctaca g 21

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<400> 93  
aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
<211> 23  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaaggg gatatatcgc cac 23

<210> 95  
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<400> 95  
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<212> DNA  
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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200  
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 aaaaaaaaaa aaaaaa 1016

<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 20 25 30  
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
 35 40 45  
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
 50 55 60  
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
 65 70 75  
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys



	80	85	90
Thr Gly Pro Ile	Gly Lys Lys Gly Asp 95	Lys Gly Glu Lys Gly 100	Leu 105
Leu Gly Ile Pro	Gly Glu Lys Gly Lys 110	Ala Gly Thr Val Cys 115	Asp 120
Cys Gly Arg Tyr	Arg Lys Phe Val Gly 125	Gln Leu Asp Ile Ser 130	Ile 135
Ala Arg Leu Lys	Thr Ser Met Lys Phe 140	Val Lys Asn Val Ile 145	Ala 150
Gly Ile Arg Glu	Thr Glu Glu Lys Phe 155	Tyr Tyr Ile Val Gln 160	Glu 165
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr 170	His Cys Arg Ile Arg 175	Gly 180
Gly Met Leu Ala	Met Pro Lys Asp Glu 185	Ala Ala Asn Thr Leu 190	Ile 195
Ala Asp Tyr Val	Ala Lys Ser Gly Phe 200	Phe Arg Val Phe Ile 205	Gly 210
Val Asn Asp Leu	Glu Arg Glu Gly Gln 215	Tyr Met Ser Thr Asp 220	Asn 225
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp 230	Asn Glu Gly Glu Pro 235	Ser 240
Asp Pro Tyr Gly	His Glu Asp Cys Val 245	Glu Met Leu Ser Ser 250	Gly 255
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Glu Phe Ile Lys	Lys Lys Lys 275		

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 <210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
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<223> Synthetic oligonucleotide probe

<400> 99  
gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

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 <211> 730  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45	
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60	
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75	
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90	
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105		
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120	
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135	
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150	
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165	
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180	
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195	
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210	

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Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

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500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp 515	Pro Gln Gly His Cys Met 520	
Ala Thr Ser Pro Gly Glu Pro Gly Leu 530	Leu Val Ala Pro Val Ser 535	
Gln Gln Ser Pro Phe Leu Gly Tyr Ala 545	Gly Gly Pro Glu Leu Ala 550	
Gln Gly Lys Leu Leu Lys Asp Val Phe 560	Arg Pro Gly Asp Val Phe 565	
Phe Asn Thr Gly Asp Leu Leu Val Cys 575	Asp Asp Gln Gly Phe Leu 580	
Arg Phe His Asp Arg Thr Gly Asp Thr 590	Phe Arg Trp Lys Gly Glu 595	
Asn Val Ala Thr Thr Glu Val Ala Glu 605	Val Phe Glu Ala Leu Asp 610	
Phe Leu Gln Glu Val Asn Val Tyr Gly 620	Val Thr Val Pro Gly His 625	
Glu Gly Arg Ala Gly Met Ala Ala Leu 635	Val Leu Arg Pro Pro His 640	
Ala Leu Asp Leu Met Gln Leu Tyr Thr 650	His Val Ser Glu Asn Leu 655	
Pro Pro Tyr Ala Arg Pro Arg Phe Leu 665	Arg Leu Gln Glu Ser Leu 670	
Ala Thr Thr Glu Thr Phe Lys Gln Gln 680	Lys Val Arg Met Ala Asn 685	
Glu Gly Phe Asp Pro Ser Thr Leu Ser 695	Asp Pro Leu Tyr Val Leu 700	
Asp Gln Ala Val Gly Ala Tyr Leu Pro 710	Leu Thr Thr Ala Arg Tyr 715	
Ser Ala Leu Leu Ala Gly Asn Leu Arg 725	Ile 730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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ggagaatgtg gccacaac 18

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<210> 107  
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ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
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<212> DNA  
<213> Homo sapiens

<400> 108  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
 65 70 75

09078299 "101501

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
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Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
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Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
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0997899-10501

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Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu		
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Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile		
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Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met		
455	460	465
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<400> 111

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

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<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

09978299-101501

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Asn Cys Leu Pro Leu Asp Asn Ala Thr 155	Leu Pro Gln Lys Leu Lys 160	Lys 165
Glu Val Gly Tyr Ser Thr His Met Val 170	Gly Lys Trp His Leu Gly 175	Gly 180
Phe Asn Arg Lys Glu Cys Met Pro Thr 185	Arg Arg Gly Phe Asp Thr 190	Thr 195
Phe Phe Gly Ser Leu Leu Gly Ser Gly 200	Asp Tyr Tyr Thr His Tyr 205	Tyr 210
Lys Cys Asp Ser Pro Gly Met Cys Gly 215	Tyr Asp Leu Tyr Glu Asn 220	Asn 225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn 230	Gly Ile Tyr Ser Thr Gln 235	Gln 240
Met Tyr Thr Gln Arg Val Gln Gln Ile 245	Leu Ala Ser His Asn Pro 250	Pro 255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala 260	Tyr Gln Ala Val His Ser 265	Ser 270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe 275	Glu His Tyr Arg Ser Ile 280	Ile 285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala 290	Ala Met Leu Ser Cys Leu 295	Leu 300
Asp Glu Ala Ile Asn Asn Val Thr Leu 305	Ala Leu Lys Thr Tyr Gly 310	Gly 315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr 320	Ser Ser Asp Asn Gly Gly 325	Gly 330
Gln Pro Thr Ala Gly Gly Ser Asn Trp 335	Pro Leu Arg Gly Ser Lys 340	Lys 345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg 350	Ala Val Gly Phe Val His 355	His 360
Ser Pro Leu Leu Lys Asn Lys Gly Thr 365	Val Cys Lys Glu Leu Val 370	Val 375
His Ile Thr Asp Trp Tyr Pro Thr Leu 380	Ile Ser Leu Ala Glu Gly 385	Gly 390
Gln Ile Asp Glu Asp Ile Gln Leu Asp 395	Gly Tyr Asp Ile Trp Glu 400	Glu 405



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 Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
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 Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
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<210> 118  
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 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900  
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950  
 caatatattgc tttaaatatc atatcactgt atcttctcag tcatttctga 2000  
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 cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100  
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 <211> 338  
 <212> PRT  
 <213> Homo sapiens

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09978269-101501

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro				

305

310

315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
 320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 120

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&lt;210&gt; 121

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 121

ggctgcacgt atggctatcc atag 24

&lt;210&gt; 122

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 122

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&lt;210&gt; 123

&lt;211&gt; 1199

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

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 <213> Homo sapiens

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 35 40 45  
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
 50 55 60  
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90

Thr Lys His Asp

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<223> Synthetic oligonucleotide probe

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<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaattg 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131

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 <212> PRT  
 <213> Homo sapiens

<400> 132  
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                     20                    25                    30  
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
                     35                    40                    45  
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
                     50                    55                    60  
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
                     65                    70                    75

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Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

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365	370	375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His Gly
380	385	390
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu Leu
395	400	405
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu Cys
410	415	420
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly Trp
425	430	435
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu Gln
440	445	450
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg Leu
455	460	465
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly Met
470	475	480
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly Leu
485	490	495
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe Leu
500	505	510
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala Arg
515	520	525
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val Ser
530	535	540
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro Glu
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Cys		

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<211> 45

<212> DNA

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<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

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 <213> Homo sapiens

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 <221> unsure  
 <222> 233  
 <223> unknown amino acid

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
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Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
	50	55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
	65	70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
	80	85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
	95	100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
	110	115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
	125	130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
	140	145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
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Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
	170	175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
	185	190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
	200	205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
	215	220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
	230	235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
	245	250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
	260	265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
	275	280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
	290	295	300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile  
 305 310 315

Ala

<210> 138  
 <211> 24  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
 ctggcacagc tcaacctcat ctgg 24

<210> 139  
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<220>  
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<400> 139  
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<210> 140  
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<220>  
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<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24  
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<220>  
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<400> 141  
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<210> 142  
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 <212> DNA  
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<220>  
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<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
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<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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tacgttctta aatctatgaa gtcgagggac ctttcgctgc ttttgtaggg 150  
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 aggcggaggt tgcagtgage caagattgtg ccactgcact ccagcctggg 2250  
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 145

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				20					25					30
Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
				35					40					45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
				50					55					60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
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Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
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Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
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Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
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Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
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Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
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Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
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Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
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Leu

<210> 146  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 146  
ctttccttgc ttcagcaaca tgaggc 26

<210> 147  
<211> 25  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 147  
gcccagagca ggaggaatga tgagc 25

<210> 148  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 148  
gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149  
<211> 2196  
<212> DNA  
<213> Homo sapiens

<400> 149  
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 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

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 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 150

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Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp	35	40	45	
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His	50	55	60	
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys	65	70	75	
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu	80	85	90	
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro	95	100	105	
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu	110	115	120	
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg	125	130	135	
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu	140	145	150	
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser	155	160	165	
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val	170	175	180	
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp	185	190	195	
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro	200	205	210	
Asp	Asp	Gly	Ala	Lys	215													

<210> 151

<211> 524  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 103, 233  
<223> unknown base

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ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcc 200  
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tgagacgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450  
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caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgcccg 100  
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ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
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<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
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<210> 155  
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<400> 155  
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<210> 156  
<211> 2680  
<212> DNA  
<213> Homo sapiens

<400> 156  
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 <211> 412  
 <212> PRT  
 <213> Artificial

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 Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
 35 40 45  
 Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
 50 55 60  
 Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
 65 70 75  
 Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
 80 85 90  
 Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
 95 100 105  
 Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

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Thr Phe Ser Leu Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val Gly	
125	130	135
Ser Tyr Phe His Thr Met Val Glu Ser	Leu Val Gly Trp Gly Tyr	
140	145	150
Thr Arg Gly Glu Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg Arg	
155	160	165
Ala Pro Asn Glu Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu Met	
170	175	180
Ile Glu Glu Met Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu Val	
185	190	195
Ala His Ser Met Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln Arg	
200	205	210
Gln Pro Gln Ala Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val Ser	
215	220	225
Leu Gly Ala Pro Trp Gly Gly Val Ala	Lys Thr Leu Arg Val Leu	
230	235	240
Ala Ser Gly Asp Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu Lys	
245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu Leu	
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln Thr	
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe Gln	
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr Glu	
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His Cys	
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr Glu	
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly Asp	
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp Gln	
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly Ser	
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr Leu	
395	400	405

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

cgagcgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50

atggagagcg gggcctacgg cgcggccaaag gcgggcggct ccttcgacct 100

gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150

tcttcgcctt gatcgtgttc tcttgcattc atggtgaggg ctacagcaat 200

gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250

ctgccgctat ggcagtgcc tgggggtgct ggccttcctg gcctcggcct 300

tcttcttggt ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350

cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

0908299-101501

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 ccaactccga ccccaacact gcctacgcct cctacccagg tgcattctgtg 650  
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700  
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 cctgtgcccga gagggttca gtcagccgct cactcctcca gggcactttt 950  
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 gtgcccctat gctccagac tctgtctgtg ccgagtgtat tataaaatcg 1450  
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 tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100					105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
				155					160					165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr	
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<210> 163  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 tggtcttcgc cttgatcgtg ttct 24

<210> 164  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggtga tggctgccct cac 23

<210> 166  
<211> 23  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
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agggtgatca gtgagcagaa ggatgccgt ggccgaggcc cccaggtgg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150  
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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
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tttgaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169  
<211> 802  
<212> PRT  
<213> Homo sapiens  
<400> 169

09978299-101501

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

09978299-101501

290	295	300
Val Val Trp Lys	Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val	
305	310	315
Leu Ser Val Gln	Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu	
320	325	330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro	
335	340	345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His	
350	355	360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	
365	370	375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln	
380	385	390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile	
395	400	405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly	
410	415	420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly	
425	430	435
Val Arg Val His	Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro	
440	445	450
Gly Glu Phe Leu	Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys	
455	460	465
Asp Gly Val Lys	Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys	
470	475	480
Val Cys Arg Ala	Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile	
485	490	495
Ser Leu Pro Lys	Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly	
500	505	510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe	
515	520	525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro	
530	535	540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu	
545	550	555
His Cys Asp Cys	Gly Leu Gln Gly Pro Ser Ser Arg Ile Val Gly	
560	565	570
Gly Ala Val Ser	Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu	
575	580	585

09978299-101501

Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln	Val Val Thr		800		

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 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150  
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaaccgcga gtgtgatggg cgccccgact gcagggacgg ctccgatgag 500  
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550  
 agctgtgtcc tccgaggggtg agtggccatg gcagggcagc ctccaggttc 600  
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 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 172  
taatccagca gtgcaggccg gg 22

<210> 173  
<211> 50  
<212> DNA  
<213> Artificial Sequence

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<400> 173  
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<210> 174  
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tgcctatgca ctgaggaggc agaag 25

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
aggcagggac acagagtcca ttcac 25

<210> 176  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
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<210> 177  
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<212> DNA  
<213> Homo sapiens

<400> 177

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ctccagtccc ccagcccctg gccgagagaa gggctttacc ggccgggatt 150  
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ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250  
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agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450  
tgcagtttca acatgacagc taaaaccttt ttcatcattc acggatggac 500  
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cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700  
tcgggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750  
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tcttgccggg cccatgtttg aaggggccga catccacaag aggtctctctc 850  
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ggcttgagca ttggtattca gatgcctgtg ggccacattg acatctaccc 950  
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gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100  
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agaagtggcc agcacaatcc aatcaaatcg ttgcaaata gattacactg 1400  
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aataaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr  
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Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
20 25 30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val  
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val  
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val  
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro  
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser  
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
230 235 240

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Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	245	250	255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	260	265	270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	275	280	285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser	290	295	300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	305	310	315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	320	325	330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	335	340	345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro							350		

<210> 179  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 179  
 gtgagcatga gcgagccgtc cac 23

<210> 180  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 180  
 gctattacaa cggttcttgc ggcagc 26

<210> 181  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 181  
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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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cgagccacct cttccctccc cccgcttccc tgtcgcgctc cgctggctgg 100  
acgcgctgga ggagtggagc agcaccgggc cggccctggg ggctgacagt 150  
cggcaaagt tggcccgaag aggaagtggg ctcaaaccgc ggcaggtggc 200  
gaccaggcca gaccaggggc gctcgtgcc tgcgggcccg ctgtaggcga 250  
gggcgcgccc cagtgcgag acccggggct tcaggagccg gcccggggag 300  
agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350  
caccgcccct actccgggc tgcgcgcc tccccgccc cagccctggc 400  
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ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550  
gttgccacc ctctctccc tctccttgg aggcgctctg gccatccag 600  
accggattat ttttccaaat catgcttgat aggaccccc agcagtgtc 650  
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tcaccatcag gttccagaag ctacacctgg cctgtggctc agagcgctta 800  
accctacgt cccctctcca gccactgatc tccctgtgtg aggcacctcc 850  
cagccctctg cagctgcccg ggggcaacgt caccatcact tacagctatg 900  
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 gttctgcccc gcaaggtcat tacagctgca gtcattggca gcctagtgtg 1900  
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 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro			

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	170		175		180
Gly Leu Thr Pro	Arg 185	Pro Val Pro Ser	Leu 190	Pro Cys Asn Val	Thr 195
Leu Glu Asp Phe	Tyr 200	Gly Val Phe Ser	Ser 205	Pro Gly Tyr Thr	His 210
Leu Ala Ser Val	Ser 215	His Pro Gln Ser	Cys 220	His Trp Leu Leu	Asp 225
Pro His Asp Gly	Arg 230	Arg Leu Ala Val	Arg 235	Phe Thr Ala Leu	Asp 240
Leu Gly Phe Gly	Asp 245	Ala Val His Val	Tyr 250	Asp Gly Pro Gly	Pro 255
Pro Glu Ser Ser	Arg 260	Leu Leu Arg Ser	Leu 265	Thr His Phe Ser	Asn 270
Gly Lys Ala Val	Thr 275	Val Glu Thr Leu	Ser 280	Gly Gln Ala Val	Val 285
Ser Tyr His Thr	Val 290	Ala Trp Ser Asn	Gly 295	Arg Gly Phe Asn	Ala 300
Thr Tyr His Val	Arg 305	Gly Tyr Cys Leu	Pro 310	Trp Asp Arg Pro	Cys 315
Gly Leu Gly Ser	Gly 320	Leu Gly Ala Gly	Glu 325	Gly Leu Gly Glu	Arg 330
Cys Tyr Ser Glu	Ala 335	Gln Arg Cys Asp	Gly 340	Ser Trp Asp Cys	Ala 345
Asp Gly Thr Asp	Glu 350	Glu Asp Cys Pro	Gly 355	Cys Pro Pro Gly	His 360
Phe Pro Cys Gly	Ala 365	Ala Gly Thr Ser	Gly 370	Ala Thr Ala Cys	Tyr 375
Leu Pro Ala Asp	Arg 380	Cys Asn Tyr Gln	Thr 385	Phe Cys Ala Asp	Gly 390
Ala Asp Glu Arg	Arg 395	Cys Arg His Cys	Gln 400	Pro Gly Asn Phe	Arg 405
Cys Arg Asp Glu	Lys 410	Cys Val Tyr Glu	Thr 415	Trp Val Cys Asp	Gly 420
Gln Pro Asp Cys	Ala 425	Asp Gly Ser Asp	Glu 430	Trp Asp Cys Ser	Tyr 435
Val Leu Pro Arg	Lys 440	Val Ile Thr Ala	Ala 445	Val Ile Gly Ser	Leu 450
Val Cys Gly Leu	Leu 455	Leu Val Ile Ala	Leu 460	Gly Cys Thr Cys	Lys 465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu
				470					475					480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser
				485					490					495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp
				500					505					510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu
				515					520					525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly
				530					535					540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg
				545					550					555
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn
				560					565					570
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser
				575					580					585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg
				590					595					600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro
				605					610					615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala
				620					625					630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro
				635					640					645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly
				650					655					660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro
				665					670					675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp
				680					685					690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu
				695					700					705
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr							
				710										

- <210> 184
- <211> 20
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgcctgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50  
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100  
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
tgcggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350  
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atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450  
agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600  
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
aaaaaaaaaa aaa 663

<210> 190  
<211> 152  
<212> PRT  
<213> Homo sapiens

<400> 190  
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Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val  
20 25 30  
Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr  
35 40 45  
Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile  
50 55 60  
Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe  
65 70 75  
Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe  
80 85 90  
Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr  
95 100 105  
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys  
110 115 120  
Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn  
125 130 135  
Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150



Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
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ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgccctt tctgtttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaaat gngacatcta tgaccttttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
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gcctttgctt gatattatca actcactggt aacaacagta ttcatgctca 400  
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ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
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cactggcccg ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150  
gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200  
cgcggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300  
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agaagctaca gattctcggt gacactggaa gcagtaactt tgccgtggca 450  
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cttgcccggt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850  
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900  
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950  
aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000  
acagtggcac cacgctgctg cgcccgcccc agaaggtgtt tgatgcgggtg 1050  
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<210> 196  
 <211> 518  
 <212> PRT  
 <213> Homo sapien

<400> 196  
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 Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr  
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 Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro  
 35 40 45  
 Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu  
 50 55 60  
 Ala Leu Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala  
 65 70 75  
 Asn Phe Leu Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg  
 80 85 90  
 Gly Tyr Tyr Leu Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu  
 95 100 105

Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	335	340	345
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu			

395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly	Phe Tyr Val Ile Phe Asp	
410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala Glu	
425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser Thr	
440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser Glu	
455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala	Leu Met Ser Val Cys Gly	
470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu	Leu Leu Leu Pro Phe Arg	
485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu	Val Val Asn Asp Glu Ser	
500	505	510
Ser Leu Val Arg His Arg Trp Lys		
515		

<210> 197  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 197  
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<210> 198  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 198  
 ggaaattgga ggccaaagc 19

<210> 199  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 ggatgtagcc agcaactgtg 20

<210> 200  
 <211> 19  
 <212> DNA  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 200  
 gccttggtc gttctcttc 19  
  
 <210> 201  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 201  
 ggtcctgtgc ctggatgg 18  
  
 <210> 202  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 202  
 gacaagacta cctccgttg tc 22  
  
 <210> 203  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 203  
 tgatgcacag ttcagcacct gttg 24  
  
 <210> 204  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 204  
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 <210> 205  
 <211> 1939  
 <212> DNA

<213> Homo sapiens

<400> 205

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gggggggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200  
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 cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850  
 ttccgggcgg atgcagggct ggggtcatct gtatctgaag cccctcggaa 1900  
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
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 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
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 35 40 45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
 50 55 60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
 65 70 75  
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
 80 85 90  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
 95 100 105  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
 110 115 120  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
 125 130 135  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
 140 145 150



His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val
				155					160					165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe
				170					175					180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg
				185					190					195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu
				200					205					210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala
				215					220					225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro
				230					235					240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu
				245					250					255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu
				260					265					270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys
				275					280					285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala
				290					295					300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro
				305					310					315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser
				320					325					330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr
				335					340					345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser
				350					355					360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln
				365					370					375

Leu Ser

<210> 207  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 207  
 cttcatggcc ttggacttgg ccag 24

<210> 208  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
<211> 45  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 209  
ctttctgagc tctgagccac ggttgacat cctcatccac aatgc 45

<210> 210  
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<212> DNA  
<213> Homo sapiens

<400> 210  
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 tacagatata ccagtgagga tgccatccta aaacacagga tggatcacag 1550  
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aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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			20						25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

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Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420
Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr	425	430	435
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala	440	445	450
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val	455	460	465
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly	470	475	480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met	485	490	495
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr	500	505	510
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg	515	520	525
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu			

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530										535					540				
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp					
				545					550					555					
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser					
				560					565					570					
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu					
				575					580					585					
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp					
				590					595					600					
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu					
				605					610					615					
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln					
				620					625					630					
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu					
				635					640					645					
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser					
				650					655					660					
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala					
				665					670					675					
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg					
				680					685					690					
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr					
				695					700					705					
Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser					
				710					715					720					
Ser	Ile	Leu	Leu	Pro	Ala	Ala	Pro	Ile	Pro	Ile	Leu	Ser	Pro	Cys					
				725					730					735					
Ser	Pro	Pro	Ser	Pro	Gln	Ala	Ser	Ser	Leu	Ser	Gly	Pro	Ser	Pro					
				740					745					750					
Ala	Ser	Ser	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Leu	Gly	Glu					
				755					760					765					
Asp	Gln	Asp	Ser	Val	Leu	Thr	Pro	Glu	Glu	Val	Ala	Leu	Cys	Leu					
				770					775					780					
Glu	Leu	Ser	Glu	Gly	Glu	Glu	Thr	Pro	Arg	Asn	Ser	Val	Ser	Pro					
				785					790					795					
Met	Pro	Arg	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Gly	Tyr	Ile	Ser					
				800					805					810					
Val	Pro	Thr	Ala	Ser	Glu	Phe	Thr	Asp	Met	Gly	Arg	Thr	Gly	Gly					
				815					820					825					

Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	830	835	840
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	845	850	855
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	860	865	870
Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	875	880	885
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	890	895	900
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	905	910	915
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	920	925	930
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	935	940	945
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	950	955	960
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	965	970	975
Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						980	985	

<210> 212  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 212  
 gaagggacct acatgtgtgt ggcc 24  
  
 <210> 213  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 213  
 actgaccttc cagctgagcc acac 24  
  
 <210> 214  
 <211> 50  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctgggt 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agcccccagg 500

attgacttct cctgggctct acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggccct ccattgccag ggacttccca gtacggggcac 600

gaaaggactt ctcagtacac aggaacctct cctcaccag cgacctctcc 650

tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggcctgatcg cttctgcag ccacctgctc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcgaggga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000

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tctogaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050  
cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100  
cacctcagcc tcagagtcca gctgcccga ctccagggtc ctccccaccc 1150  
tccccaggct ctctcttgc atgttccagc ctgacctaga agcgtttgtc 1200  
agccctggag cccagagcgg tggccttgc ctccgggtg gagactggga 1250  
catccctgat aggttcacat cctggggcag agtaccaggc tgctgaccct 1300  
cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350  
aggaactcct gggcctcatg cccagtgtcg gaccctgcct tcctcccact 1400  
ccagacccca ccttgtcttc cctccctggc gtcctcagac ttagtccac 1450  
ggctctcctgc atcagctggg gatgaagagg agcatgctgg ggtgagactg 1500  
ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550  
gtgaaaaacg tgattcctgg cccaccaag acccaccaa accatctctg 1600  
ggcttggtgc aggactctga attctaaca tgcccagtga ctgtgcact 1650  
tgagtttgag ggccagtggg cctgatgaac gtcacaccc ctccagctta 1700  
gagtctgcat ttgggctgtg acgtctccac ctgcccgaat agatctgctc 1750  
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caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850  
acagaagtgg ttgcctttnc catttgcct cctgggncca tgccttcttg 1900  
cctttggaaa aaatgatgaa gaaaaccttg gtccttcct tgtctggaaa 1950  
gggttacttg cctatgggtt ctggtggcta gagagaaaag tagaaaacca 2000  
gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050  
ctgaaggtga ctccgagtc agccccctgg agaaggggtc gggggtggtg 2100  
gtaaagtagc acaactacta ttttttttct tttccatta ttattgtttt 2150  
ttaagacaga atctcgtgct gctgcccagg ctggagtga gtggcacgat 2200  
ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250  
gagtagctgg gattacaggc acgcaccacc acacctggct aatttttgta 2300  
cttttagtag agatgggggtt tcacatggtt ggccaggctg gtcttgaact 2350  
cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400  
caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450

agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500  
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
 ttgtgtgtac ttccttccac tcttttcttc ttcacataat ttgccggtgt 2600  
 tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650  
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly  
 1 5 10 15  
 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly  
 20 25 30  
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
 35 40 45  
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
 50 55 60  
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met  
 65 70 75  
 Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu  
 80 85 90  
 Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr  
 95 100 105  
 Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile  
 110 115 120  
 Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser  
 125 130 135  
 Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala  
 140 145 150  
 Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu  
 155 160 165  
 Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu  
 170 175 180  
 Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr  
 185 190 195  
 Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala 215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg 230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu 245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His 260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln 275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys 290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro 305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val 320	325	330

Ser Ala

- <210> 217
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 217
- ccctgcagtg cacctacagg gaag 24
- <210> 218
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 218
- ctgtcttccc ctgcttggt gtgg 24
- <210> 219
- <211> 47
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 219  
gggtgcaggaa gggtgggata ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgtctctg ttgccaggc tagagtgtac 150  
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggggc tccacctctg 350  
ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400  
gctgggatca tgttgttggc cctggctctgt ctgctcagct gcctgctacc 450  
ctccagttag gccaagctct acggtcgttg tgaactggcc agagtgtac 500  
atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
gggtgcagcaa cctcaccccg aacgtcccca acgtgtgccg gatgtactgc 700  
tcagatttgt tgaatcctaa totcaaggat accgttatct gtgccatgaa 750  
gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 221  
Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
1 5 10 15  
Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
                     35                    40                    45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
                     50                    55                    60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
                     65                    70                    75  
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
                     80                    85                    90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
                     95                    100                    105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
                     110                    115                    120  
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
                     125                    130                    135  
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
                     140                    145

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 gggatcatgt tgttggccct ggtc 24

<210> 223  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
 gcaaggcaga cccagtcagc cag 23

<210> 224  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 224  
 ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggcccggg cggccgcggc ggcacccatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tctcgtctt cgcgctcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcatgga ctcgggtgcgc cgcggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctcttc ggcaagggtg tgacgcaagg 350  
gactcgggag ggggccttcg tgtacgccat ctcttcggca ggtgtggcct 400  
ttgcagtgc gcgggctgac agcagtgggg agctggagaa gtgcggctgt 450  
gacaggacag tgcatggggc cagcccacag ggcttcacgt ggtcaggatg 500  
ctctgacaac atcgctacg gtgtggcctt ctacacagtcg tttgtggatg 550  
tgcgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttcgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcca ctgagggtgga gccacgccgc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga ggggcccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000  
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350

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gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400  
 acctaaggtg gagtaacaag gattattacc accacatggc tactgaccgt 1450  
 gtcacgctggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
 tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaagt 1600  
 ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
 tcagccctta catggacagc tagagggtcg atatctgtgg gtccttcag 1700  
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
 cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccg 1850  
 gctgtgcctt tgcagtcagt cccgagtcac tttcacagc gctgttcctc 1900  
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
 ctgtgccttt gcagtcagt cccgagtcac tttcacagca ctgttcctc 2049

<210> 226  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 226  
 Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
 1 5 10 15  
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
 20 25 30  
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
 35 40 45  
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
 50 55 60  
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
 65 70 75  
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
 80 85 90  
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
 95 100 105  
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
 110 115 120



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Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 227  
 gctgcagctg caaattccac tgg 23

<210> 228  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 228  
tgggtgggaga ctgttttaa t tatcggcc 28

<210> 229  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 229  
tgcttcgtca agtgccggca gtgccagcgg ctctggagt t 41

<210> 230  
<211> 1355  
<212> DNA  
<213> Homo sapiens

<400> 230  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50  
gggtgcctgc atcgccatgg acaccaaccag gtacagcaag tggggcgga 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200  
ggctgtgatt ctgagtatcc tattgtccaa ggccctccacg gagcgcgcg 250  
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300  
gcggcgctgg gtgcctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500  
cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550  
gcgagccgtg cccacgctg tggctgtcct tcgagggtc ctgctacttt 600  
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650  
tgccagcgcg cacctgggtga tcgttggggg cctggatgag cagggttcc 700  
tcactcgaa cacgcgtggc cgtgggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgcccagtg ccttgagacc gcgcccattg cagcatgtcg tatcctgggg 1000  
gctgctcacc tccctggctc ctggagctga ttgccaaaga gtttttttct 1050  
tcctcatcca ccgctgctga gtctcagaaa cacttggtccc aacatagccc 1100  
tgtccagccc agtgctggg ctctgggacc tccatgccga cctcatccta 1150  
actccactca cgcagacca acctaacctc cactagctcc aaaatccctg 1200  
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggtag 1250  
gtgactgagg actggagctg tttggtttct tcgcattttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaa 1355

<210> 231  
<211> 293  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
1 5 10 15  
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
20 25 30  
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
35 40 45  
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
50 55 60  
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
65 70 75  
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
80 85 90  
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105  
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120  
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg
				140					145					150
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys
				155					160					165
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser
				170					175					180
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp
				185					190					195
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly
				200					205					210
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 232  
 gcgagaactg tgtcatgatg ctgc 24  
  
 <210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 233  
 gtttctgaga ctcagcagcg gtgg 24  
  
 <210> 234  
 <211> 50  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctcctccttt 100

ctccacgctc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccgggcg cggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgct gtcctgccc ggtgatggaa aaccccagcc cggccgccc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgcccgc 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tcccaagca 450

gtacccctg ttccgcccc ctgcgcagtg gtcttogctg ctgggggccc 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggccc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700

cagcgcaggc actcgctggt ctcgtttggt gtgcgcacgt tgcccagccc 750

cgactggttc gtgggctggt acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca ccttctctc cccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccaccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggtgcgac agagccccag ggccttcac cctccgccc cagtccctgcc 1050

cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccc 1100

09578399 "101501

tggactgoga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150  
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 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250  
 tccctgataa ctgctgtctaa gaccagagcc ccgcagcccc tggggccccc 1300  
 cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
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 cgaccatctc tgactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctcttttccc aaccttgctt cttagggggc cccgtgtccc 1500  
 gtctgtcttc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctgggtccc acgtggttgc agatacctca 1650  
 gacctggtgc tctaggtgt gctgagccca ctctcccgag ggcgcatcca 1700  
 agcggggggcc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75  
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val

	110	115	120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly	Gln
	125	130	135
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val	Ser
	140	145	150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly	Val
	155	160	165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln	Ala
	170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly	Phe
	185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr	Val
	200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser	Phe
	215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val	Thr
	230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro	Ala
	245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala	Ser
	260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser	Ser
	275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys	Ser
	290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser	Pro
	305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn	Cys
	320	325	330

Val

- <210> 237
- <211> 22
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 237
- cagcactgcc aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 238  
 caggactcgc tacgtccg 18  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 239  
 cagcccccttc tctcctttc tccc 24  
  
 <210> 240  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 240  
 gcagttatca gggacgcact cagcc 25  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 241  
 ccagcgagag gcagatag 18  
  
 <210> 242  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 cggtcaccgt gtcctgcggg atg 23  
  
 <210> 243  
 <211> 42  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagcccccttc tctctctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50  
tgtcttgcggt gatattgaca aactgaagct ttcctgcacc actggactta 100  
aggaagagtgt tactcgtagg cggacagctt tagtgccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtgggtcc aaagaagctc ctaaagcttg 300  
cagaaatddd atccaacttt gtttggaagc ttattatgac aataccattd 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500  
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggtda caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
gaccacataa tccacacaaa ataaaaagct gtgaggtdtt gtttaatcct 700  
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750  
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattdtagtt 800  
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaattga 850  
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atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000  
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050  
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
 agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
 tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250  
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 tcacatgtac ttcagtttga ggataaaaagc agaaaagtga aagatgcaag 1500  
 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
 ataaaagaag gaggggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
 agaagataaa atgagaataa tgataaccag aacttgctgg aatgtgcct 1650  
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
 gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750  
 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850  
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
 <211> 472  
 <212> PRT  
 <213> Homo sapiens

<400> 245  
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
 1 5 10 15  
 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
 20 25 30  
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
 35 40 45  
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
 50 55 60  
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
 65 70 75  
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
 80 85 90  
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
 95 100 105

Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala	110	115	120
Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly	125	130	135
Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu			

FOSTOT 66282660

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met		
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp		
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg		
440	445	450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met		
455	460	465
Arg Glu Lys Lys Glu Arg Arg		
470		

<210> 246  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 246  
 tgcggagatc ctactggcac aggg 24

<210> 247  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 247  
 cgagtttagtc agagcatg 18

<210> 248  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 248  
 cagatggtgc tgttgccg 18

<210> 249  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 249  
caactggaac aggaactgag atgtggatc 29

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctggttcagc agtgcaagg tctg 24

<210> 251  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
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gatgctgccc ggcccgctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtogagccct ggccagacat gtccacaggg 150  
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200  
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250  
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactocagca 300  
actacatctg ctccttcaag tggttttgga accgggctct ttggatctaa 350  
acctgccact gggttcactc taggaggaac aaatacaggt gccttgacaca 400

ccaagaggcc tcaagtggc accaaatatg gaaccctgca aggaaaacag 450  
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccctctc 500  
cagacctoct ctaggatatcc tcagggttgc acctccagaa cccccggagc 550  
cctggaaagg aatcagagat gctaccacct acccgcttg atggagtctc 600  
gctctgtgc caggctggag tgcagtggca cgatctcggc tcaactgcaac 650  
ctccgcctcc cgggttcaag cgagtctoct gcctcagcct ctgagtgtct 700  
ggggctacag gtgcctgcag gagtctctgg gccagctggc ctcgatgtac 750  
gtcagcacgc gggaacggta caagtggctg cgcttcagcg aggactgtct 800  
gtacctgaac gtgtacgcgc cggcgcgcg gcgcggggat cccagctgc 850  
cagtgatggc ctggttcccg ggaggcgct tcatcgtgg cgctgcttct 900  
tcgtacgagg gctctgactt ggccgcccgc gagaaagtgg tgctggtgtt 950  
tctgcagcac aggctcggca tcttcggctt cctgagcacg gacgacagcc 1000  
acgcgcgcgg gaactggggg ctgctggacc agatggcggc tctgcgctgg 1050  
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gttcggccag tcggcggggg ccatgagcat ctcaggactg atgatgtcac 1150  
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gcctgagggc actatcagg accaaggtga tgcgtgtgtc caacaagatg 1350  
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agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650  
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 <211> 545  
 <212> PRT  
 <213> Homo sapiens

<400> 254  
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 20 25 30  
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 35 40 45  
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
 50 55 60  
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
 65 70 75  
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
 80 85 90  
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
 95 100 105  
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
 110 115 120  
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
 125 130 135

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Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145			150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160			165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175			180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190			195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205			210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220			225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235			240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250			255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265			270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280			285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295			300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310			315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325			330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340			345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355			360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370			375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385			390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400			405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415			420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro					



425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu		
440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn		
455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp		
470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met		
485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr		
500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala		
515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu		
530	535	540
Pro Gln Glu Trp Ala		
545		

<210> 255  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 255  
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<210> 256  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 256  
 ccacctcagg aagccgaaga tgcc 24

<210> 257  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 257  
 gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258  
<211> 2764  
<212> DNA  
<213> Homo sapiens

<400> 258  
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ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150  
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200  
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
acccgggggc gattccagct cactggggat cccgccaagg ggaactgctc 350  
cttggtgata agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
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caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
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aatcggcatc acggctcttc ttttctctg cctggccctg atcatcatga 1300

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 cccctcctcc accagggtgct ccctccccag aatcaaagaa gaaccagaaa 1500  
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 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700  
 ctatggagta gccattcttt tgttccttta cttctttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln  
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20 25 30  
Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45  
Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60  
Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75  
Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90  
Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105  
Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120  
Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135  
Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150  
His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165  
Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180  
Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195  
Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210  
Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225  
Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240  
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

09078299 101501

Lys	Ala	Gly	Asp	Ser	Gly	Arg	Tyr	Thr	Cys	Arg	Ala	Glu	Asn	Arg	
				260					265					270	
Leu	Gly	Ser	Gln	Gln	Arg	Ala	Leu	Asp	Leu	Ser	Val	Gln	Tyr	Pro	
				275					280					285	
Pro	Glu	Asn	Leu	Arg	Val	Met	Val	Ser	Gln	Ala	Asn	Arg	Thr	Val	
				290					295					300	
Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
				305					310					315	
Gln	Ser	Leu	Cys	Leu	Val	Cys	Val	Thr	His	Ser	Ser	Pro	Pro	Ala	
				320					325					330	
Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
				335					340					345	
Pro	Ser	Asp	Pro	Gly	Val	Leu	Glu	Leu	Pro	Arg	Val	Gln	Val	Glu	
				350					355					360	
His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
				365					370					375	
Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
				380					385					390	
Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
				395					400					405	
Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
				410					415					420	
Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
				425					430					435	
Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
				440					445					450	
Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
				455					460					465	
Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
				470					475					480	
Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
				485					490					495	
Pro	Lys	Ser	Ser	Thr	Gln	Ala	Pro	Glu	Ser	Gln	Glu	Ser	Gln	Glu	
				500					505					510	
Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
				515					520					525	
Pro	Glu	Ala	Arg	Met	Pro	Lys	Gly	Thr	Gln	Ala	Asp	Tyr	Ala	Glu	
				530					535					540	
Val	Lys	Phe	Gln												

<210> 260  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 260  
 caaagcctgc gcctggtctg tg 22

<210> 261  
 <211> 24  
 <212> DNA  
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<220>  
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<400> 261  
 ttctggagcc cagaggggtgc tgag 24

<210> 262  
 <211> 45  
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<220>  
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<400> 262  
 ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263  
 <211> 2857  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
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 caacagaaaa ctctcaaaa aagaaagtca agcagccagt gcgatctcat 150  
 ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200  
 aatgaatacg actagtcac acatcggcc gctaagatct gatttagaca 250  
 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
 acttttatca ttgatgaaag aacagggtgac atatatgcc tacagaagct 350  
 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
 tcgctactgg aagggtgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
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caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
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cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700  
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750  
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800  
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ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900  
gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950  
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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 20 25 30

Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
 35 40 45

Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
 50 55 60



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His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn	65	70	75
Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe	80	85	90
Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu	95	100	105
Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile	110	115	120
Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val	125	130	135
Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp	140	145	150
Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr	155	160	165
Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser	170	175	180
Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro	185	190	195
Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser	200	205	210
Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln	215	220	225
Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr	230	235	240
Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile	245	250	255
Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro	260	265	270
Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile	275	280	285
Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln			

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350	355	360
Val Glu Asp Val	Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr	
365	370	375
Val Phe Glu Val	Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly	
380	385	390
Val Val Ser Ala	Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg	
395	400	405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly	
410	415	420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp	
425	430	435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln	
440	445	450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp	
455	460	465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu	
470	475	480
Asn Ala Gly Ser	Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp	
485	490	495
Arg Asp Glu Ser	Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser	
500	505	510
Val Glu Asp Thr	Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln	
515	520	525
Asp Asn Thr Ala	Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu	
530	535	540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn	
545	550	555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val	
560	565	570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln	
575	580	585
Glu Leu Val Leu	Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala	
590	595	600
Ile Leu Ile Cys	Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr	
605	610	615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys	
620	625	630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly	
635	640	645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

<400> 265  
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50  
 gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100  
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200  
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgcgcgcgc gggcgcgagc 50

cccaaccccg accagagct tctccagcgg cggcgcgagc agcagggctc 100

ccgccttaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gccacctgc aaactctccg cttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcag ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gcatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttgga tcctcctggg agtgatagca 500

atctttgtgg ccaccgttg catgaagtgt atgaagtgc tggaagacga 550

tgagggtgcag aagatgagga tggctgtcat tgggggtgcg atattttctc 600

ttgcaggctt ggctatttta gttgccacag catggtatgg caatagaatc 650  
 gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700  
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttctgg 750  
 gaggtgccct actttgctgt tctgtcccc gaaaaacaac ctcttaccca 800  
 acaccaaggc cctatccaaa acctgcacct tccagcgga aagactacgt 850  
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900  
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000  
 gttaaaatac tcagtgcata acatggctta atcttatttt atcttctttc 1050  
 ctcaatatag gaggaagat tttccattt gtattactgc ttccattga 1100  
 gtaatcatat tcaaatgggg gaaggggtgc tcttaaata tatatagata 1150  
 tgtatatata catgtttttc tattaataat agacagtaaa atactattct 1200  
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
 atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300  
 ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350  
 tttgggtgcc tttgccacaa gacctagcct aatttaccac ggatgaattc 1400  
 tttcaattct tcatgcgtgc cttttcata tacttatttt attttttacc 1450  
 ataattctat agcacttgca tctgtattaa gcccttattt gttttgtgtt 1500  
 tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550  
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600  
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650  
 ccctgtactc tgacccatag cactcttggt tgctttgaaa atatttgtcc 1700  
 aattgagtag ctgcatgctg ttccccagg tgttgtaaca caactttatt 1750  
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800  
 ctttttgttc cccattcctt aattgtattg ttttccaag tgtaattatc 1850  
 atgcgtttta tatcttcta ataagggtgtg gtctgtttgt ctgaacaaag 1900  
 tgctagactt tctggagtga taatctggtg acaaatattc tctctgtagc 1950  
 tgtaagcaag tcaactaatc tttctacctc tttttctat ctgccaaatt 2000  
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

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105707 6582680

tttatattac tcttattctt tgaacatgaa ctatgcctat gtagtgtctt 2100  
tatttgctca gctggctgag aactgaaga agtcactgaa caaaacctac 2150  
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctatctt 2200  
ccactgaaca aaacctacac acataccttc atgtggttca gtgccttcct 2250  
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300  
gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350  
gtgtctgaca tgtttgtgct ctgttccatt ttaacaactg ctcttacttt 2400  
tccagtctgt acagaatgct atttcacttg agcaagatga tgtaatggaa 2450  
aggggtgttg cactggtgtc tggagacctg gatttgagtc ttggtgctat 2500  
caatcacctg ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550  
cttcactgtg aagcgggtgg ttgtaattcc tgatcttccc acctcacagt 2600  
gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtaag 2747

<210> 270  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 270  
Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe  
1 5 10 15  
Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp  
20 25 30  
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala  
35 40 45  
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly  
50 55 60  
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser  
65 70 75  
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu  
80 85 90  
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met  
95 100 105  
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val  
110 115 120

Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val
				125					130					135
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp
				140					145					150
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu
				155					160					165
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala
				170					175					180
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr
				185					190					195
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr
				200					205					210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
 ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttctctg 50  
 ggatggatcg ggcgcatcnt cacactgccc ttccccagtg gaggatttta 100  
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150  
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatgggtgt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg ggcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450  
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggcctctctt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttctctg tccc 564

<210> 272  
 <211> 498

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<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
<223> unknown base

<400> 272  
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50  
tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150  
acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200  
tcgcagagca cggggcagat ccagtgcaaa gtctttgact cccttgctga 250  
atctgagcag cacattgcaa gcaacccgtg ccttgatggt ggttggcatc 300  
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtga 350  
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgaga tatttcttct tgcaggtctg gctatttttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273  
gggcccgaacc attatccaac cgggntcaact gttggctcat ctccctcctg 50  
gatgaanccg gccatcntca gactccctgc cccatggaga tttnnccat 100  
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgetgaatct gngcagcaca ttgcagcaac cntgccctg atggtgggtg 250  
gcatectcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgaatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450



cccagtc aat gccaggtacg aatttgggtca ggctctcttc actgggtggg 500  
 ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
 attctcccct cctggatgga tcgcnccacc gtcacattgc cttccccan 50  
 tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtgc aaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caaccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttggga agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnngnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450  
 tcaggtcttc ttcactggct gggtgctgc ttctctctgc cttctgggag 500  
 gtgccctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
 gcagcacatt ncaagcaacc ccttgccctg aagtggttg ncatcccccc 100  
 tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
 tgccaggtac gaatttggtc aggctctctt cactggctgg gctgctgctt 350  
 ctctctgcoct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
 <223> unknown base

<400> 276  
 agcaatgccc tgccccagt ggaggattaa ttcctatgnt ggggacaaca 50  
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgctgtcgc 100  
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtgggtt ggcattcttc 200  
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
 cgcgatattt ctntttgcag gtctggctat tttagttgcc acagcatggt 350  
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400  
 gccaggtacg aatttgggtc ggctttnttc actggctggg ctgctgcttn 450  
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 87, 138, 147, 163, 165-166, 172  
 <223> unknown base

<400> 277  
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 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100  
 cccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150  
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcctgggat ggatccgccc ccatcntcac atgccctgcc cnttgagat 50  
ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150  
aagtctttga ctcttgctg aatctgagca gcacattgca agcaacntg 200  
ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250  
accgttggca tgaagtgtg tgaagtgctt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350  
gctatttttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400  
tctatgaccc tatgaccca gtcaatgccg ggtacgaatt tggtcaggct 450  
ctcttcactg gctgggctgc tgcttctctc tgccttctgg gaggtgccct 500  
actttgctgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcatctcgc ttctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gacncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200  
aatctgagca gcacattgca agcaacntg ccttgatggt ggttggcatc 250  
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttgctgtt cctgcgaa 548

<210> 280  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 280  
 cgagcgagtc atggccaacg c 21

<210> 281  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 281  
 gtgtcacacg tagtccttcc cgctgg 26

<210> 282  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 282  
 ctgcagctgt tgggcttcat tctcgcttc ctgggatgga tcg 43

<210> 283  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 283  
 gcgtgccgtc agctcgccgg gcaccgcggc ctgcacctcg ccctccgccc 50  
 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccaccccg 100  
 tagaggaccc ccgcccgtgc cccgaccggt ccccgcttt ttgtaaaact 150  
 taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
 ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

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ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcatc aaagacagaa acaccaatag tgtctaagtc 700  
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgtagaggta gcatgcacag gatggtaaat tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050  
aattaatgta tgatgacatc tcacaggctt tgcctttaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
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ctttattaat gacaaggga accatgagta atgccacaat ggcatttgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctgcctgt tgggtgctggc ccttggggag 1350  
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acgtggccca ctcccgccc aggtgcttt ccgtgtcttc agttctgtcc 1450  
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ctctggagag tctggatcatg tggagggtggg gtttattggg atgctggaga 1850  
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900  
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950  
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gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag ttgactgtg aattaatttt 2200  
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250  
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284  
<211> 243  
<212> PRT  
<213> Homo sapiens

<400> 284  
Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu  
1 5 10 15  
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu  
20 25 30  
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys  
35 40 45  
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile  
50 55 60  
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro  
65 70 75  
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val  
80 85 90  
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val  
95 100 105  
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg  
110 115 120  
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val  
125 130 135  
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr  
140 145 150

09978299-101504

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu	
				155					160					165	
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val	
				170					175					180	
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly	
				185					190					195	
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala	
				200					205					210	
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu	
				215					220					225	
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys	
				230					235					240	

Ile Ala Leu

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 40, 53, 68, 119, 134, 177-178, 255  
 <223> unknown base

<400> 285  
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 ctggagtcag gacaatggnt cgggctgcag aggnnttagaa gcgagggcac 150  
 cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200  
 cttctagtag tagttgagag tttgactgtg aattaatttt atgccataaa 250  
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
 gttaacttta aatgagc 418

<210> 286  
 <211> 543  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 73, 97

099829-101501

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttgga catgatgctg 50  
gattacctcc ttaaatagaca ccnttcctcg cctgttggtg ctggccnttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag cttaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcattctatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

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ctttagtagagg tagnatgcac cnggctggtg aattggattg gtggatccac 100  
catatccatg ggattttaaat ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base



<400> 288  
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 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
 actgattgac ccagcgcttt ggaaataaat ggcaagtgtt tgttcantta 200  
 aagggaccaa gctaaatttg tattgggttca ttagtggaag tcaaactgtt 250  
 attcagagat gtttaattgca tattaantt atttaattga tttatntca 300  
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tctctgtct 400  
 ttggagagtc tggcatgtg gaggtggg 428

<210> 289  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50  
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
 tactcgtcat aagtgaagg cgtgtgttga ctgattgacc cagcgctttg 150  
 gaaataaatg gcagtgtttt gttcacttaa agggaccaag ctaaatttgt 200  
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaattgat 250  
 atttaactta tttaattgat ttcattcat gttttcttat tgtcacaaga 300  
 gtacagttaa tgctgcgtgc 320

<210> 290  
 <211> 609  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
 447, 481, 513, 532, 584, 598  
 <223> unknown base

<400> 290  
 aaacctttaa aagttgagg gaaaagaatg atcctttatt aatgacaagg 50  
 gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100  
 ttggtaggcc ttggtacatg atgctggatt acctctctta aatgacacc 150  
 cttctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300  
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
 cagangtant ngtcataagt gagaggcgtg tggtgantga ttgaccagc 400  
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
 atttgattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
 acaagggtag agttaatgct gcgtgctgct gaantctgtt gggagaantg 600  
 gtattgctg 609

<210> 291  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
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 cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100  
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
 gagaggcgtg tggtgactga ttgaccagc gctttggaaa taaatggcag 250  
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 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400  
 gcgtgctgct gaactctgtt gggagaactg gtattgctgc tggagggctg 450  
 tgggctcttc tgtctctgga gagtctggc atgtggaggt ggg 493

<210> 292  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 292  
 gcaccaccgt aggtacttgt gtgagc 27

<210> 293  
 <211> 23  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150  
gtctcacttt gttgccagg ctggagttca gtgccatgat catggtttac 200  
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250  
acaggacaaa attagaagat caaatggaa aatatgctgc tttggttgat 300  
atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350  
attttatgtg gcaacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450  
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cctagtttag aaatagggaa gctgagacat ttaagatct caagttttta 2250  
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<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp	1	5	10	15
Thr	Leu	Ile	Asp	Gly	Ser	Glu	Met	Glu	Trp	Asp	Phe	Met	Trp	His	20	25	30	
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu	35	40	45	
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr	50	55	60	
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu	65	70	75	
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn	80	85	90	
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu	95	100	105	
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg	110	115	120	
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp	125	130	135	
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu	140	145	150	
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu	155	160	165	
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly	170	175	180	
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser	185	190	195	
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala	200	205	210	

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
 215 220 225  
 Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
 230 235 240  
 Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
 245 250 255  
 Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
 260 265 270  
 Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
 275 280 285  
 His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
 290 295 300  
 Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
 305 310 315  
 Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
 320 325 330  
 Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
 335 340 345  
 Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
 350 355 360  
 Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
 365 370 375  
 Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
 380 385 390  
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 395 400 405  
 Asn Asp Ala Asn Cys Ala Tyr Gly  
 410

<210> 297  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 297  
 gcatctgcag gagagagcga aggg 24  
  
 <210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcggtccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggaggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
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 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650  
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700  
 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750  
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800  
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850  
 ttagtttcaa aaaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe  
 1 5 10 15  
 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
 20 25 30  
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
 35 40 45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
 50 55 60



Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr	65	70	75
Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala	80	85	90
Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe	95	100	105
Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser	110	115	120
Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala	125	130	135
Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro			

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggcgcgt 100  
 ctggggcggg cgctgtggct ggcggcccg cggttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcgggtc agctccgcgc cgagctccgc caggccgcgcg 350  
 agtgccggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgtc gcgctcgggt cgcgcccttct gccaggaaat 450

gctccaggaa gagcctagge tggatgtctt gatcaataac gcagggatct 500  
 tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcaactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaaactg gctaacattc tttttaccag 750  
 ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900  
 agtagaaggt gccagactt ccatttattt ggccctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggtt ggccgtgctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatatgtta aaattataac tgggcaagca 1350  
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 303  
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15  
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30  
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	320	325	330
Met	Val	Gly	Leu	Leu	Lys												

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atgggtngcc tgctaaaata 100  
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250  
 actgaaaaat tttttttggg ataagagaat ttcagcaaag atgtttttaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

09976299-101504

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 307  
aacgcaggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308  
<211> 1523  
<212> DNA  
<213> Homo sapiens

<400> 308  
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150  
cttctatcc ttaccgacc tcagatgctc cttctgctc ctgtaactt 200  
gggtttttac tctgtaca actgaaataa caagtcttg tacagagaat 250  
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaatttt gaggaagctt 350  
ccgatgtcat taaggaagaa ttccaaatg aaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttctcttgt cggagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttcat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250  
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctcttccag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser
1				5					10					15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu
				20					25					30
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn
				35					40					45
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe
				50					55					60
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile
				65					70					75
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val
				80					85					90
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser
				95					100					105
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys
				110					115					120
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr
				125					130					135
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu
				140					145					150
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly
				155					160					165

06978299-101501

Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg  
170 175 180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe  
185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile  
200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly  
215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys  
230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu  
245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys  
260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg  
275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp  
290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro  
305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr  
320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys  
335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe  
350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala  
365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu  
380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu  
395 400 405

Leu

<210> 310  
<211> 182  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> unsure



<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgcgcngg agcccgggtc 50  
gagaggacna ggtgccgtg cctggagaat cctccgtgc cgtcgggtcc 100  
cggagcccag ccctttccta acccaacca acctagccn gtcccagccg 150  
ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttctatcc ttaccgcacc tcagatgctc cttctgctc ctggtaac'tt 250  
gggtttttac tctgtaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactgggtg cgtttcagtc agatgtggca tccaat'tttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaa't tg'tttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctggaagt tg 22

09978299-10501  
F05T01"66282660

<210> 313  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 313  
 gtcagcgatc agtgaaagc 19  
  
 <210> 314  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 314  
 ccagaatgaa gtagctcggc 20  
  
 <210> 315  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 315  
 ccgactcaaa atgcattgtc 20  
  
 <210> 316  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 316  
 catttggcag gaattgtcc 19  
  
 <210> 317  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 317  
 ggtgctatag gccaaagg 18  
  
 <210> 318  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgttttcccta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgtgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600  
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa ctgactcttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgct ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt cttaagcata agtaaactg atataaaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactct gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
 110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
 125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
 140

<210> 323  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
 tgtaataccc tgaatcccct tgtactocca gactaccta tccacgcttt 100  
 cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtotca 150  
 atatgcccct cttggcatat catatttga ggtatatgag tagaccagt 200  
 atgagtggcc caggactcta tgacctaca accatcatga atgcagatat 250  
 tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
 tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
 tagaacaaca cacagaagaa ttggtccagt taagtgcag caaaaagcca 400  
 ccaaataag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
 gaatctgatc agttacttta aaaaatg 477

<210> 324  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 324  
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 325  
 caggaaacag ctatgaccac ctgcacacct gcaaatacat t 41

<210> 326

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150  
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgctt tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550  
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
 aactcttgct ctctcggtga tggattgct ttggatttgt tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat ctgctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
 caaataaagt tactcaaate tgtg 1174

<210> 330  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 330  
 Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly  
 1 5 10 15  
 Leu Pro Pro Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser  
 20 25 30  
 Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr  
 35 40 45  
 Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr  
 50 55 60  
 Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg  
 65 70 75  
 Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn  
 80 85 90  
 Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser  
 95 100 105  
 Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
 110 115 120

09978299-101504

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ttgggtgata cggcgtcttg ccaccggggc tgtcagttga cctaccctt 50  
 gcacacctac cctaaggaag aggagttgta cgcatgtcag agaggttgca 100  
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaactga 150  
 actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200  
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250



aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300

tttctctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 47

<223> unknown base

<400> 332

cacactggcc ggatctttta gaggcctttg accttgacca agggctcngga 50

aaacagcaac aagctgagct gctgtgacag aggaacaag atggcggcgc 100

cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150

tgctgaccat ggccctggcc ggaggttcgg ggaccgcttc ggctgaagca 200

tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250

gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300

agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350

gacttaaata gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400

ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450

tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgcaaaaa 500

atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550

gatggactcc gc 562

<210> 333

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 333

acaagctgag ctgctgtgac ag 22

<210> 334

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

09070209.101501

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggtt ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcattctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccc cggtctggga ttcttggttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaacct tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
agccacagac aattaaaga cctttaaatc ctttggtctt tgggtcaaggg 850  
acaagtgaag agaactttt ttacagttgg ctagaaggtc tctgtgtaga 900  
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatctt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200  
 acttctggaa atacttcacg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcatttttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgcgtctgtt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac attttttaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtgg 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
 1 5 10 15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
 20 25 30  
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
 35 40 45  
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
 50 55 60  
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
 65 70 75

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Tyr Tyr Lys Val	Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln		95	100	105
Ser Asp Glu Val	Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala	Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala	Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln	Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp	Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn	Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile	Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile	Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu	Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys	Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His	245	250	255
Ala Ser Ile Asn	Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu	Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp	Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu	Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315
Ser Lys Val Leu	Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe	320	325	330
Thr Gly Asn Lys	Ile Gln Asp Glu Glu Asn Lys Met Leu Leu Leu	335	340	345
Glu Ile Leu His	Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu	350	355	360
Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys				

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp				
	380		385		390
Cys Val Gly Cys	Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr				
	395		400		405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu				
	410		415		420
Ile Ala Asn Met	Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu				
	425		430		435
Thr Arg Gln Glu	Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile				
	440		445		450
Ser Thr Ser Val	Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln				
	455		460		465

Asn Ile His

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50  
 ttaaaagacc tttaaatacct ttggcttctg gtcaaggagac aagtgaagag 100  
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350  
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400  
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaat 450  
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500  
 tttgctg 507

<210> 339  
 <211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 339  
aagctgccgg agctgcaatg 20

<210> 340  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 340  
ttgcttctta atcctgagcg c 21

<210> 341  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 341  
aaaggaggac tttcgactgc 20

<210> 342  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 342  
agagattcat ccaactgctcc aagtcg 26

<210> 343  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 343  
tgtccagaaa caggcacata tcagc 25

<210> 344  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cgacagcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50  
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100  
ggacttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtttcct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttgat acagtgtctt acaacatgtt gggggtggac agcgatggat 300  
gctgggtggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350  
tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450  
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tgagctaagg agaggggtgt ggcagtgtct ctgaaggtcc ataaaagaaa 550  
aaagagaagt gtggtgaagg aaaatgggtc gtgtggaggg gtcaaggagt 600  
taaaaacctt agaaagcaaa aggtaggtaa tgtcaggagg tagtcttcat 650  
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700  
gtaactatth ccccatccc caggcctgtg cccctctctg gtctcgtgct 750  
tgtggcagct ctgtcttcag ttctgggata tgtgccctgt tggatgcttc 800  
attccagcct caggggaagcc tggcaccac tgccaacgt gagccagagg 850  
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc taccctcatt 950  
gctacctaag gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggg 1050  
caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150

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gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200  
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450  
 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
 1 5 10 15  
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
 20 25 30  
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347



cacagttccc caccatcact cntcccatte cttccaactt tatttttagc 50  
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
 ggagaggggac agaggccaga ggactttctca tactggacag aaaccgatca 150  
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttctt 200  
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300  
 gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350  
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400  
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
 tggatgatgg 509

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 348  
 agggacagag gccagaggac ttc 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 349  
 caggtgcata ttcacagcag gatg 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 350  
 ggaactcccc ttctgcaact acctgttctt gccctggtg ttcct 45

<210> 351  
 <211> 2056  
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctggggt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
gcttcctggg cgggtcttag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctacaaaa 250  
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ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
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 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
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 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
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 1 5 10 15  
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
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 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120

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Thr Ser Ala Trp	Ser Ile Leu Lys His	Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr	Arg Pro Gly Met Glu	Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile	Glu Leu Glu Asp Leu	Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr	Trp Arg Arg Glu Pro	Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg	Ser Gly Gly Ile Pro	Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala	Ala Tyr Cys Val Lys	Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg	Tyr Ser Ala Phe Ser	Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu	Ala Ile Pro Leu Val	Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met	Leu Ile Leu Val Val	Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg	Leu Leu Gln Tyr Ser	Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr	Leu Lys Ile Thr Asn	Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg	Glu Glu Val Asp Ala	Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu	Leu Leu Arg Ala Trp	Ile Ser	305	310	

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
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 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctcaactcact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggccca 550  
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
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 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggccaata 800  
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
 ggcgctgggt tgat 864

<210> 354  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 354  
 aggcttcgct gcgactagac etc 23

<210> 355  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 355  
 ccaggtcggg taaggatggt tgag 24

<210> 356  
 <211> 50  
 <212> DNA  
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<220>  
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tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
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acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
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agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agaggaaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500  
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550  
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ataatctcca gggaaacttc gtgccagggc ctcttttctg gggcctggtg 750  
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tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900  
catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950  
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 ttaaaggac agaatactta 1670

<210> 358  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 358

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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp	20	25	30	
Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe	35	40	45	
Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser	50	55	60	
Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	65	70	75	
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	80	85	90	
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	95	100	105	
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	110	115	120	
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	125	130	135	
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	140	145	150	
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	155	160	165	
Glu	Leu	Tyr	Gly	Asn	Phe	Ser	Ala	Ala	Ser	Arg	Gly	Pro	Asn	Gly				

170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn		
185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile		
200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu		
215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser		
230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile		
245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg		
260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser		
275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg		
290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro		
305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg		
320	325	
<210> 359		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Synthetic oligonucleotide probe		
<400> 359		
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<223> Synthetic oligonucleotide probe		
<400> 360		
gaggctctgg aagatctgag atgg 24		
<210> 361		
<211> 50		
<212> DNA		
<213> Artificial Sequence		



<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

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gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200  
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363

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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25						30
Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu
				35				40						45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn
				50				55						60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln
				65				70						75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val
				80				85						90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp
				95				100						105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu
				110				115						120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln
				125				130						135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His
				140				145						150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys
				155				160						165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly

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170	175	180
Cys Ala Ile Asn Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile	
185	190	195
Trp Pro Lys Ala Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly	
200	205	210
Asn Trp Trp Gly His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser	
215	220	225
Ala Cys Pro Pro Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys	
230	235	240
Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu	
245	250	255
Thr Asn Glu Ile Glu Arg Gln Gln Ser	Gln Val His Asp Thr His	
260	265	270
Val Arg Thr Arg Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser	
275	280	285
Ala Gln Gln Met Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg	
290	295	300
Asp Gln Cys Lys Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala	
305	310	315
Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr	
320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile	
335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg	
350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile	
365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr	
380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro	
395	400	405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg	
410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr	
425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His	
440	445	450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro	
455	460	465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
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Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
 485 490 495

Val Phe Ala Val Val  
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<210> 364  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 364  
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<210> 365  
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 <212> DNA  
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<220>  
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<400> 365  
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<210> 366  
 <211> 25  
 <212> DNA  
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<220>  
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<400> 366  
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<210> 367  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 367  
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<210> 368  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

09978299 101501

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

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gcatgaggct cctggcggcc gcgctgctcc tgetgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400

cgaggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450

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agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550

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TOPOL 65282660

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 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 370  
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 35 40 45  
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 50 55 60  
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
 65 70 75  
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
 80 85 90  
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys  
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 Arg Arg Val Tyr Glu Glu  
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 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

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<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc ccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tggatgaagac gaagatatc atgatcagaa cagtaagaag 550

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tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000  
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aaacgagatt attccaccga attaagtgtc accattgccg tcggggcgctc 2100

09978299 "101501

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agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050  
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taagagactt tgt 3113

<210> 375  
<211> 816  
<212> PRT  
<213> Homo sapiens

<400> 375  
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20 25 30  
Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn  
35 40 45  
Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala

10578299 "101501

50	55	60
Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro		
65	70	75
Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val		
80	85	90
Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu		
95	100	105
Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val		
110	115	120
Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro		
125	130	135
Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr		
140	145	150
Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser		
155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu		
170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly		
185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly		
200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu		
215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly		
230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly		
245	250	255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser		
260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu		
275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile		
290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met		
305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln		
320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile		
335	340	345

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Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

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Asn	Pro	Lys	His	Ser	Lys	Asp	Pro	His	Lys	Thr	Gly	Pro	Glu	Asp
				650					655					660
Thr	Thr	Val	Leu	Ile	Glu	Thr	Lys	Arg	Asp	Tyr	Ser	Thr	Glu	Leu
				665					670					675
Ser	Val	Thr	Ile	Ala	Val	Gly	Ala	Ser	Leu	Leu	Phe	Leu	Asn	Ile
				680					685					690
Leu	Ala	Phe	Ala	Ala	Leu	Tyr	Tyr	Lys	Lys	Asp	Lys	Arg	Arg	His
				695					700					705
Glu	Thr	His	Arg	Arg	Pro	Ser	Pro	Gln	Arg	Asn	Thr	Thr	Asn	Asp
				710					715					720
Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
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His	Ser	Thr	Thr	Arg	Val									
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 <223> Synthetic oligonucleotide probe

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<210> 377  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ggccgcatg g 2461

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<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly	
				35					40					45	
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro	
				50					55					60	
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met	
				65					70					75	
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp	
				80					85					90	
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe	
				95					100					105	
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln	
				110					115					120	
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr	
				125					130					135	
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys	
				140					145					150	
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu	
				155					160					165	
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn	
				170					175					180	
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr	
				185					190					195	
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp	
				200					205					210	
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met	
				215					220					225	
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val	
				230					235					240	
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser	
				245					250					255	



Ile Thr Gly Asp	Leu Ser Asp Asn His	Asp Val Ile Ser Leu Lys
260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu	
275	280	285
His Arg Asp Val Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro	
290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe	
305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val	
320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys	
335	340	345

Arg Phe Tyr

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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 381  
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<210> 382  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 382  
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<210> 383  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 383  
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<210> 384  
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 <212> DNA  
 <213> Homo sapiens

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<400> 384

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 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150  
 tgggggtctgg ctcagaattc ctgcagctgg tgaaaatctg ttttctagaa 200  
 gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250  
 ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300  
 tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350  
 cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
 caagagtcga aagagaatca tgcccgaacc tgtgacggag ccccctgtga 450  
 cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500  
 gagcgagca tggaagggtca tgccccgcat cattttaagc tgggtctcagt 550  
 gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600  
 aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650  
 tatcacccaa aactggaagc tttcattagt cacatgtcaa aaggatccgg 700  
 agcctctttc gaaagcccct tgaactcctt gcctctttac ccaaaccacc 750  
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 gctgtagttt gctgaccct catctaaaa ataggctata ctacaattgc 2400  
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 tgatttctga actaatgggtg ctaattcaga gaaatggaaa gtgaaagtga 3050  
 gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100  
 gtgttgcaatt tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile	20	25	30	
Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys	35	40	45	
Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro	50	55	60	
Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu	65	70	75	
Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser	80	85	90	
Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val	95	100	105	
Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala	110	115	120	
Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His	125	130	135	
Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser	140	145	150	
Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu	155	160	165	
Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu	170	175	180	
Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp	185	190	195	
Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr	200	205	210	

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Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe	215	220	225
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	230	235	240
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	245	250	255
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	260	265	270
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	275	280	285
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	290	295	300
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	305	310	315
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	320	325	330
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	335	340	345
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	350	355	360
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	365	370	375
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	380	385	390
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	395	400	405
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	410	415	420
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	425	430	435
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	440	445	450
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	455	460	465
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	470	475	480

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 <212> DNA  
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<220>  
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<400> 386  
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<210> 387  
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<220>  
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<400> 387  
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<210> 388  
<211> 50  
<212> DNA  
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<210> 389  
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atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccctg 200  
cacgcgcctg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250  
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 <211> 916  
 <212> PRT  
 <213> Homo sapiens  
 <400> 390



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Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val	35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala	50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe	65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile	80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn	95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu	110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu	125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met	140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn	155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu	170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val	185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu	200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr	215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu	245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp	260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp	275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr				

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290										295					300				
Ile	Ser	Thr	Ile	Gly	Glu	Leu	Asp	His		Glu	Glu	Ser	Gly	Phe	Tyr				
				305											315				
Gln	Met	Glu	Val	Gln	Ala	Met	Asp	Asn		Ala	Gly	Tyr	Ser	Ala	Arg				
				320											330				
Ala	Lys	Val	Leu	Ile	Thr	Val	Leu	Asp		Val	Asn	Asp	Asn	Ala	Pro				
				335											345				
Glu	Val	Val	Leu	Thr	Ser	Leu	Ala	Ser		Ser	Val	Pro	Glu	Asn	Ser				
				350											360				
Pro	Arg	Gly	Thr	Leu	Ile	Ala	Leu	Leu		Asn	Val	Asn	Asp	Gln	Asp				
				365											375				
Ser	Glu	Glu	Asn	Gly	Gln	Val	Ile	Cys		Phe	Ile	Gln	Gly	Asn	Leu				
				380											390				
Pro	Phe	Lys	Leu	Glu	Lys	Ser	Tyr	Gly		Asn	Tyr	Tyr	Ser	Leu	Val				
				395											405				
Thr	Asp	Ile	Val	Leu	Asp	Arg	Glu	Gln		Val	Pro	Ser	Tyr	Asn	Ile				
				410											420				
Thr	Val	Thr	Ala	Thr	Asp	Arg	Gly	Thr		Pro	Pro	Leu	Ser	Thr	Glu				
				425											435				
Thr	His	Ile	Ser	Leu	Asn	Val	Ala	Asp		Thr	Asn	Asp	Asn	Pro	Pro				
				440											450				
Val	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Ala		Tyr	Ile	Pro	Glu	Asn	Asn				
				455											465				
Pro	Arg	Gly	Val	Ser	Leu	Val	Ser	Val		Thr	Ala	His	Asp	Pro	Asp				
				470											480				
Cys	Glu	Glu	Asn	Ala	Gln	Ile	Thr	Tyr		Ser	Leu	Ala	Glu	Asn	Thr				
				485											495				
Ile	Gln	Gly	Ala	Ser	Leu	Ser	Ser	Tyr		Val	Ser	Ile	Asn	Ser	Asp				
				500											510				
Thr	Gly	Val	Leu	Tyr	Ala	Leu	Ser	Ser		Phe	Asp	Tyr	Glu	Gln	Phe				
				515											525				
Arg	Asp	Leu	Gln	Val	Lys	Val	Met	Ala		Arg	Asp	Asn	Gly	His	Pro				
				530											540				
Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser		Leu	Phe	Val	Leu	Asp	Gln				
				545											555				
Asn	Asp	Asn	Ala	Pro	Glu	Ile	Leu	Tyr		Pro	Ala	Leu	Pro	Thr	Asp				
				560											570				
Gly	Ser	Thr	Gly	Val	Glu	Leu	Ala	Pro		Arg	Ser	Ala	Glu	Pro	Gly				
				575											585				

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Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	
				590					595					600	
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	
				605					610					615	
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	
				620					625					630	
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	
				635					640					645	
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	
				650					655					660	
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	
				665					670					675	
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	
				680					685					690	
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	
				695					700					705	
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	
				710					715					720	
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	
				725					730					735	
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	
				740					745					750	
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	
				755					760					765	
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	
				770					775					780	
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	
				785					790					795	
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	
				800					805					810	
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	
				815					820					825	
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	
				830					835					840	
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	
				845					850					855	
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	
				860					865					870	
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu	

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875

880

885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro  
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

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cccagttaaa aggtccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccaactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

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 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450  
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 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550  
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 tggaggcccc ctggtgtgtg atggtgcact ccagggcata acatcctggg 850  
 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
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 ctaggataag cactagatct cccttaataa actcacaact ctctgggttc 999

<210> 395  
 <211> 260  
 <212> PRT  
 <213> Homo sapiens

<400> 395  
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 20 25 30  
 Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro  
 35 40 45  
 Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly  
 50 55 60  
 Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys  
 65 70 75  
 Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn  
 80 85 90  
 Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro  
 95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
 110 115 120  
 Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
 125 130 135  
 Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
 140 145 150  
 Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
 155 160 165  
 Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
 170 175 180  
 Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
 185 190 195  
 Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
 200 205 210  
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
 215 220 225  
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
 230 235 240  
 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
 245 250 255  
 Ile Gly Ser Lys Gly  
 260

<210> 396  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 396  
 cagcctacag aataaagatg gccc 24  
  
 <210> 397  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 397  
 ggtgcaatga tctgccaggc tgat 24  
  
 <210> 398  
 <211> 48  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaataacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccggccc gccgcgcgc ccacgcccc accccggccc gcgcccccta 100  
gccccgccc gggccgcgc ccgcgcccgc gccaggtga gcgctccgc 150  
cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200  
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250  
tcatctccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgc 300  
gccgccctcg cctgtgctgc cctgcgcgcc ctgcgcaccc gcggcccag 350  
cccagccaga gccggggcga gcggagcgcg ccgagcctcg tcccgcggcc 400  
gggcccgggc cggggcgtag cggcgcgcc tggatgcgga cccggccgcg 450  
gggagacggg cggccgcccc gaaacgactt tcagtcccc acgcgcccc 500  
cccaaccct acgatgaaga gggcgtccgc tggaggagc cggctgctgg 550  
catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccaggt 600  
gcctgcgtat gctacaatga gcccaagggt acgacaagct gccccagca 650  
gggcctgcag gctgtgccc tgggcatccc tgctgccagc cagcgcatt 700  
tctgcacgg caaccgcatt tcgcatgtgc cagctgccag cttcctgcc 750  
tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggccgaat 800  
tgatgcggct gccttactg gcctggccct cctggagcag ctggacctca 850  
gcgataatgc acagctccg tctgtggacc ctgccacatt ccacggcctg 900  
ggccgcctac acacgtgca cctggaccgc tgcggcctgc aggagctggg 950  
ccgggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000  
acaacgcgt gcaggcactg cctgatgaca cttccgcga cctgggcaac 1050  
ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagcg 1100

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cgcttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150  
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 ggccccctg cgtgccctgc agtacctgag gctcaacgac aaccctggg 1300  
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 ctggggcttc ccaagtgtg ccagccagat gccgctgaca aggcctcagt 1550  
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 aatgactcac cctttgggac tctgcctggc tctgctgagc cccgctcac 1700  
 tgcagtgcgg cccgagggct ccgagccacc aggggtcccc acctcgggcc 1750  
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 cgctggtgct gtggacagt cttgggccct gctgaccccc agcggacaca 1950  
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000  
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 tccctgatgg acgctgccc cccgccaccc ccatctccac cccatcatgt 2100  
 ttacaggggt cggcggcagc gtttgttcca gaacgccgcc tcccaccag 2150  
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200  
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400  
 <211> 473  
 <212> PRT  
 <213> Homo sapiens

<400> 400  
 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val  
 1 5 10 15  
 Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala  
 20 25 30



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Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

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320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 401  
 tggctgccct gcagtacctc tacc 24

<210> 402  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 402  
 ccctgcaggt cattggcagc tagg 24

<210> 403  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150  
agctgaatcc agcaagaaca atggaggcca gcggaagct catttgcaga 200  
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250  
cgcgggcgaa cctagaagct attctgtggt ggaggaaact gagggcagct 300  
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350  
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400  
gctcaatcag gagaccggg atttgttgct aaatgagaaa ttggaccgtg 450  
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gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050  
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cttttctgga aaatgcaccg ttctgattca agtgaatagat gtgaacgacc 1200  
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atattgtggc atttccatgc caatgtttat ttccccaat ttgtgtgtat 2650  
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 tgttttaaag tgaacattta cctttattcc tggttcctt 2738

<210> 405  
 <211> 798  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
 Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu  
 1 5 10 15  
 Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
 20 25 30  
 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
 35 40 45  
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
 50 55 60  
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
 65 70 75  
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
 80 85 90  
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
 95 100 105  
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
 110 115 120  
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
 125 130 135  
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
 140 145 150  
 Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
 155 160 165  
 Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
 170 175 180  
 Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
 185 190 195  
 Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
 200 205 210  
 Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
 215 220 225  
 Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

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230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp 245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val 260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala 275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly 290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser 305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly 320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala 335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn 350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp 365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu 380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr 395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr 410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu 425	430	435
Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala 440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser 455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser 470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp 485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn 500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln 515	520	525

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Gly Phe Gln Phe Arg Val Gly Ala Ser	Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val	Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly	Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val	Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg	Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala	Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala Ala	710	715	720
Ser Val Gly Arg Cys Leu Val Pro Glu	Gly Pro Leu Pro Gly His	725	730	735
Leu Val Asp Met Ser Gly Thr Arg Thr	Leu Ser Gln Ser Tyr Gln	740	745	750
Tyr Glu Val Cys Leu Ala Gly Gly Ser	Gly Thr Asn Glu Phe Lys	755	760	765
Phe Leu Lys Pro Ile Ile Pro Asn Phe	Pro Pro Gln Cys Pro Gly	770	775	780
Lys Glu Ile Gln Gly Asn Ser Thr Phe	Pro Asn Asn Phe Gly Phe	785	790	795

Asn Ile Gln

<210> 406

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
ctgagaacgc gcctgaaact gtg 23

<210> 407  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
agcgttgatca ttgacatcgg cg 22

<210> 408  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
<211> 1379  
<212> DNA  
<213> Homo sapiens

<400> 409  
acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50  
gcgtagccgt gcgcgattg cctctcggcc tgggcaatgg tcccggctgc 100  
cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150  
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250  
ggctgtgtac ctgggtgagg aggagctcct gcatgacccg atgggccagg 300  
acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350  
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500



cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
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 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
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 gctcttcact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
 caggtttggc accgtagctg ttcctaatat tttattattt caaggagcta 900  
 aaccaatggc cagatttaac catacagatc gaacactgga aacactgaaa 950  
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000  
 aactcaagcc gaccaaatac gccctcttcc cagcactttg ataaaaagt 1050  
 tggactggtt gcttgtattt tccttattct ttttaattag ttttattatg 1100  
 tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150  
 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200  
 ttcaatcctt cgtttcagaa attagtgcata cagtttcata cattttctcc 1250  
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
 aacaactgaa tgtataaaaa aattataaac tgggtgtttta actagtattg 1350  
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu  
 1 5 10 15  
 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val  
 20 25 30  
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
 35 40 45  
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
 50 55 60  
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
 65 70 75  
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

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80	85	90
Met Val Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val 95 100 105		
Ser Ser Glu Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu 110 115 120		
Asp Ser Arg Cys Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly 125 130 135		
Ala Gly Ala His Phe Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu 140 145 150		
Pro Glu Val Ala Glu Ser Asp Ala Ala Pro Thr Glu Asp Ser Asn 155 160 165		
Asn Thr Glu Ser Leu Lys Ser Pro Lys Val Asn Cys Glu Glu Arg 170 175 180		
Asn Ile Thr Gly Leu Glu Asn Phe Thr Leu Lys Ile Leu Asn Met 185 190 195		
Ser Gln Asp Leu Met Asp Phe Leu Asn Pro Asn Gly Ser Asp Cys 200 205 210		
Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys Arg Phe Ser Ala Ser 215 220 225		
Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala Phe Pro Ala Leu 230 235 240		
His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser Leu Ser Thr 245 250 255		
Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe Gln Gly 260 265 270		
Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu 275 280 285		
Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys 290 295 300		
Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro 305 310 315		
Ser Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu 320 325 330		
Phe Phe Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu 335 340 345		
Ser Ile Arg Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu 350 355 360		

<210> 411  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 411  
cacagagcca gaagtggcgg aatc 24

<210> 412  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 412  
ccacatgttc ctgctcttgt cctgg 25

<210> 413  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 413  
cggtagtgac tgtactctag tcctgtttta caccocgtgg tgccg 45

<210> 414  
<211> 1196  
<212> DNA  
<213> Homo sapiens

<400> 414  
cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50  
agggccctgg ctgctgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
ggctcggcgc gggggtctt cctctttggc cagcccgaact tctcctacaa 150  
gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200  
tcgaatacca gaacatgcgg ctgcccaccc tgctggggcca cgagaccatg 250  
aaggaggtgc tggagcaggc cggcgcttgg atcccgttgg tcatgaagca 300  
gtgccacccg gacaccaaga agttcctgtg ctgctcttc gccccgtct 350  
gcctcgatga cctagacgag accatccagc catgccactc gctctgcctg 400  
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gcccgaatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
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accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggt 750  
gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
tcaacgcgcc ctatctggtc atgggacaga aacaggggtg ggagctggtg 850  
atcacctcgg tgaagcgggtg gcagaagggg cagagagagt tcaagcgcac 900  
ctcccgagc atccgcaagc tgcagtgcta gtcccgcat cctgatggct 950  
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gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415  
<211> 295  
<212> PRT  
<213> Homo sapiens

<400> 415  
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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln  
20 25 30  
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val  
35 40 45  
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu  
50 55 60  
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln  
65 70 75  
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp  
80 85 90  
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp  
95 100 105  
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln  
110 115 120  
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro  
125 130 135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 416  
 cctggctcgc tgctgctgct c 21

<210> 417  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 417  
 cctcacaggt gcactgcaag ctgtc 25

<210> 418  
 <211> 47  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

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cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150  
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cactccagtg ggttttcggt cctctgtggc gctctcttca tcacgtttgg 900  
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cacctgctcg ctgctcgggc tgtttggctt ctcggtgggc ccctggcca 1100

tggagttggc ggtcgagtgt tccctccccg tgggggaggg ggctgccaca 1150  
 ggcatgatct ttgtgctggg gcaggccgag ggaataactca tcatgctggc 1200  
 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250  
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 ggctgtgca ccttcttcag ctgcatcctg gcggtcttct tccacacccc 1350  
 ataccggcgc ctgcaggccg agtctgggga gccccctcc acccgtaacg 1400  
 ccgtggggcg cgcagactca gggccgggtg tggaccgagg gggagcagga 1450  
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 aacatctggt ccacctgcgg gcgggggcga aagggtcct tgcgggctcc 1800  
 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420  
 <211> 560  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
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 35 40 45  
 Leu Trp Leu Ser Phe Ala Pro Val Ala Asp Val Ile Ala Glu Asp  
 50 55 60  
 Leu Val Leu Ser Met Glu Gln Ile Asn Trp Leu Ser Leu Val Tyr  
 65 70 75  
 Leu Val Val Ser Thr Pro Phe Gly Val Ala Ala Ile Trp Ile Leu  
 80 85 90  
 Asp Ser Val Gly Leu Arg Ala Ala Thr Ile Leu Gly Ala Trp Leu  
 95 100 105  
 Asn Phe Ala Gly Ser Val Leu Arg Met Val Pro Cys Met Val Val

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110	115	120
Gly Thr Gln Asn Pro Phe Ala Phe Leu Met Gly Gly Gln Ser Leu 125	130	135
Cys Ala Leu Ala Gln Ser Leu Val Ile Phe Ser Pro Ala Lys Leu 140	145	150
Ala Ala Leu Trp Phe Pro Glu His Gln Arg Ala Thr Ala Asn Met 155	160	165
Leu Ala Thr Met Ser Asn Pro Leu Gly Val Leu Val Ala Asn Val 170	175	180
Leu Ser Pro Val Leu Val Lys Lys Gly Glu Asp Ile Pro Leu Met 185	190	195
Leu Gly Val Tyr Thr Ile Pro Ala Gly Val Val Cys Leu Leu Ser 200	205	210
Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala 215	220	225
Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys 230	235	240
Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys 245	250	255
Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu 260	265	270
Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly 275	280	285
Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu 290	295	300
Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala 305	310	315
Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe 320	325	330
Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala 335	340	345
Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val 350	355	360
Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly 365	370	375
Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile 380	385	390
Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu 395	400	405



Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
530 535 540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

<210> 421  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
agcttctcag ccctcctgga gcag 24

<210> 422  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 422  
cgggtcaata aacctggacg cttgg 25

<210> 423  
<211> 43  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

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tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150  
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aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250  
tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300  
tctgaatcta gcccaacttg cggttaagcat gatgcaactt ctgcaacttc 350  
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caaacatgca gaactcatag tggatgaagga gctggacagg gaaatccatt 950  
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tcaggtagca gcttggtaaa ggtcaacgtc ttggactcca atgacaatag 1050  
ccctgcgttt gctgagagtt cactggcact ggaaatccaa gaagatgctg 1100

cacctggtac gcttctcata aaactgaccg ccacagaccc tgaccaaggc 1150  
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 gctggacacc ttcagtattg atgccaagac aggccaggtc attctgcgtc 1250  
 gacctctaga ctatgaaaag aacctgcct acgaggtgga tgttcaggca 1300  
 agggacctgg gtcccaatcc tatccagcc cattgcaaag ttctcatcaa 1350  
 ggttctggat gtcaatgaca acatcccaag catccacgtc acatgggcct 1400  
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 aaatataccc tcaactctgtt agcccaagac caaggactcc agcccttattc 1650  
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 <212> PRT  
 <213> Homo sapiens

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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val  
 35 40 45  
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg  
 50 55 60  
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu  
 65 70 75  
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg  
 80 85 90  
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu  
 95 100 105  
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His  
 110 115 120  
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe  
 125 130 135  
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu  
 140 145 150  
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly  
 155 160 165  
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe  
 170 175 180  
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu  
 185 190 195

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Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe Phe
200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	
215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	
230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	
245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	
260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	
275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	
290	295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn	
305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn	
320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu Ile Lys Val Leu Asp Val	
335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro	
350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu	
365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly His Asn Gly Leu Val His	
380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr	
395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg	
410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln	
425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile	
440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr	
455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile	
470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val	

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485	490	495
Ser Tyr Arg Ile Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile	
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Asp Ser Asn Thr Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	
515	520	525
Glu Glu Met Ala Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	
530	535	540
Gly Gln Pro Met Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	
545	550	555
Leu Asp Ala Asn Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	
560	565	570
Ser Asp Gly Lys Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	
575	580	585
Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	
590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	
605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	
620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	
635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	
650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	
665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	
680	685	690
Leu Arg Val Met Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	
695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	
710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	
725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	
740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	
755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	
770	775	780

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Leu Arg Gly Gln	Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785	790		795
Lys Asp Val Asp	Lys Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800	805		810
Cys Leu Gln Ala	Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815	820		825
Leu Arg Asn Gln	Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830	835		840
Val Leu Gln Asp	Thr Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845	850		855
Arg Asn Ala Ser	Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860	865		870
Ala Thr Gly Gln	Pro Arg Ser Arg Pro	Leu Lys Val Ala Gly	Ser
875	880		885
Pro Thr Gly Arg	Leu Ala Gly Asp Gln	Gly Ser Glu Glu Ala	Pro
890	895		900
Gln Arg Pro Pro	Ala Ser Ser Ala Thr	Leu Arg Arg Gln Arg	His
905	910		915
Leu Asn Gly Lys	Val Ser Pro Glu Lys	Glu Ser Gly Pro Arg	Gln
920	925		930
Ile Leu Arg Ser	Leu Val Arg Leu Ser	Val Ala Ala Phe Ala	Glu
935	940		945
Arg Asn Pro Val	Glu Glu Leu Thr Val	Asp Ser Pro Pro Val	Gln
950	955		960
Gln Ile Ser Gln	Leu Leu Ser Leu Leu	His Gln Gly Gln Phe	Gln
965	970		975
Pro Lys Pro Asn	His Arg Gly Asn Lys	Tyr Leu Ala Lys Pro	Gly
980	985		990
Gly Ser Arg Ser	Ala Ile Pro Asp Thr	Asp Gly Pro Ser Ala	Arg
995	1000		1005
Ala Gly Gly Gln	Thr Asp Pro Glu Gln	Glu Glu Gly Pro Leu	Asp
1010	1015		1020
Pro Glu Glu Asp	Leu Ser Val Lys Gln	Leu Leu Glu Glu Glu	Leu
1025	1030		1035
Ser Ser Leu Leu	Asp Pro Ser Thr Gly	Leu Ala Leu Asp Arg	Leu
1040	1045		1050
Ser Ala Pro Asp	Pro Ala Trp Met Ala	Arg Leu Ser Leu Pro	Leu
1055	1060		1065
Thr Thr Asn Tyr	Arg Asp Asn Val Ile	Ser Pro Asp Ala Ala	Ala



1070

1075

1080

Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala  
 1085 1090 1095

Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val  
 1100 1105 1110

Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser  
 1115 1120 1125

Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser  
 1130 1135 1140

Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala  
 1145 1150 1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr  
 1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu  
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&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 426

gtaagcacat gcctccagag gtgc 24

&lt;210&gt; 427

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 427

gtgacgtgga tgcttgggat gttg 24

&lt;210&gt; 428

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 428

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&lt;210&gt; 429

&lt;211&gt; 2037

<212> DNA

<213> Homo sapiens

<400> 429

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<212> PRT  
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20 25 30  
Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser  
35 40 45  
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
50 55 60  
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
65 70 75  
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
80 85 90  
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
95 100 105  
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
110 115 120

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Met Tyr Phe Phe Trp	Lys Leu Gly Asp	Pro Phe Pro Ile Leu Ser
125		130 135
Pro Lys His Gly Ile	Leu Ser Ile Glu	Gln Leu Ile Ser Arg Val
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Gly Val Ile Gly Val	Thr Leu Met Ala	Leu Leu Ser Gly Phe Gly
155		160 165
Ala Val Asn Cys Pro	Tyr Thr Tyr Met	Ser Tyr Phe Leu Arg Asn
170		175 180
Val Thr Asp Thr Asp	Ile Leu Ala Leu	Glu Arg Arg Leu Leu Gln
185		190 195
Thr Met Asp Met Ile	Ile Ser Lys Lys	Lys Arg Met Ala Met Ala
200		205 210
Arg Arg Thr Met Phe	Gln Lys Gly Glu	Val His Asn Lys Pro Ser
215		220 225
Gly Phe Trp Gly Met	Ile Lys Ser Val	Thr Thr Ser Ala Ser Gly
230		235 240
Ser Glu Asn Leu Thr	Leu Ile Gln Gln	Glu Val Asp Ala Leu Glu
245		250 255
Glu Leu Ser Arg Gln	Leu Phe Leu Glu	Thr Ala Asp Leu Tyr Ala
260		265 270
Thr Lys Glu Arg Ile	Glu Tyr Ser Lys	Thr Phe Lys Gly Lys Tyr
275		280 285
Phe Asn Phe Leu Gly	Tyr Phe Phe Ser	Ile Tyr Cys Val Trp Lys
290		295 300
Ile Phe Met Ala Thr	Ile Asn Ile Val	Phe Asp Arg Val Gly Lys
305		310 315
Thr Asp Pro Val Thr	Arg Gly Ile Glu	Ile Thr Val Asn Tyr Leu
320		325 330
Gly Ile Gln Phe Asp	Val Lys Phe Trp	Ser Gln His Ile Ser Phe
335		340 345
Ile Leu Val Gly Ile	Ile Ile Val Thr	Ser Ile Arg Gly Leu Leu
350		355 360
Ile Thr Leu Thr Lys	Phe Phe Tyr Ala	Ile Ser Ser Ser Lys Ser
365		370 375
Ser Asn Val Ile Val	Leu Leu Leu Ala	Gln Ile Met Gly Met Tyr
380		385 390
Phe Val Ser Ser Val	Leu Leu Ile Arg	Met Ser Met Pro Leu Glu
395		400 405
Tyr Arg Thr Ile Ile	Thr Glu Val Leu	Gly Glu Leu Gln Phe Asn

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
425	430	435
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Lys Gln Met Ala Pro		
455		

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 <212> DNA  
 <213> Homo sapiens

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 <223> unknown base

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 ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200



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<210> 437  
<211> 1141  
<212> PRT  
<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

80	85	90
Leu Phe Ala Cys Pro Leu Ser Leu Glu	Glu Thr Asp Cys Tyr Arg	
95	100	105
Val Asp Ile Asp Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu	
110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly	
125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val	
140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val	
155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu	
170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly	
185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His	
200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr	
215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His	
230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp	
245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser	
260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe	
275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile	
290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu	
305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val	
320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala	
335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr	
350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu	
365	370	375

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Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala	380	385	390
Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr	Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp			

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665	670	675
Gly Thr Thr Ala Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	
680	685	690
Leu Glu Leu Met Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	
695	700	705
Gln Ala Asp Gly Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	
710	715	720
Leu Pro Asp Ser Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	
725	730	735
Ala Glu Lys Pro Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	
740	745	750
Glu Cys Glu Leu Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	
755	760	765
Phe Tyr Leu Ile Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	
770	775	780
Glu Leu Glu Val Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	
785	790	795
Leu His Pro Val Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	
800	805	810
Leu Ser Ile Ala Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	
815	820	825
Gly Val Val Arg Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	
830	835	840
Gly Ser Lys Val Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	
845	850	855
Ser Leu Arg Thr Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	
860	865	870
His Glu Ile Ala Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	
875	880	885
Glu Leu Glu Gly Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	
890	895	900
Pro Arg Pro Asn Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	
905	910	915
Arg Arg Arg Glu Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	
920	925	930
Arg Gln Glu Pro Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	
935	940	945
Lys Lys Lys Asn Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	
950	955	960

Cys	Val	Val	Phe	Ser	Cys	Pro	Leu	Tyr	Ser	Phe	Asp	Arg	Ala	Ala	
				965					970					975	
Val	Leu	His	Val	Trp	Gly	Arg	Leu	Trp	Asn	Ser	Thr	Phe	Leu	Glu	
				980					985					990	
Glu	Tyr	Ser	Ala	Val	Lys	Ser	Leu	Glu	Val	Ile	Val	Arg	Ala	Asn	
				995					1000					1005	
Ile	Thr	Val	Lys	Ser	Ser	Ile	Lys	Asn	Leu	Met	Leu	Arg	Asp	Ala	
				1010					1015					1020	
Ser	Thr	Val	Ile	Pro	Val	Met	Val	Tyr	Leu	Asp	Pro	Met	Ala	Val	
				1025					1030					1035	
Val	Ala	Glu	Gly	Val	Pro	Trp	Trp	Val	Ile	Leu	Leu	Ala	Val	Leu	
				1040					1045					1050	
Ala	Gly	Leu	Leu	Val	Leu	Ala	Leu	Leu	Val	Leu	Leu	Leu	Trp	Lys	
				1055					1060					1065	
Met	Gly	Phe	Phe	Lys	Arg	Ala	Lys	His	Pro	Glu	Ala	Thr	Val	Pro	
				1070					1075					1080	
Gln	Tyr	His	Ala	Val	Lys	Ile	Pro	Arg	Glu	Asp	Arg	Gln	Gln	Phe	
				1085					1090					1095	
Lys	Glu	Glu	Lys	Thr	Gly	Thr	Ile	Leu	Arg	Asn	Asn	Trp	Gly	Ser	
				1100					1105					1110	
Pro	Arg	Arg	Glu	Gly	Pro	Asp	Ala	His	Pro	Ile	Leu	Ala	Ala	Asp	
				1115					1120					1125	
Gly	His	Pro	Glu	Leu	Gly	Pro	Asp	Gly	His	Pro	Gly	Pro	Gly	Thr	
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Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

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<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439  
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<210> 440  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 441  
<211> 1964  
<212> DNA  
<213> Homo sapiens

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ggagctgcga gcacagtgtt ggctcacaac aagatgtca aggtgtcagc 150  
cgtactgtgt gtgtgtgcag cggcttggtg cagtcagtct ctgcagctg 200  
ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250  
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300  
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400  
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aaaaaaaaaaaa 1964

<210> 442  
<211> 436  
<212> PRT  
<213> Homo sapiens

<400> 442  
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Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly  
20 25 30  
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu  
35 40 45  
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

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50	55	60
Phe Arg Asp Glu Val Glu Asp Asp Tyr	Phe Arg Thr Trp Ser Pro	
65	70	75
Gly Lys Pro Phe Asp Gln Ala Leu Asp	Pro Ala Lys Asp Pro Cys	
80	85	90
Leu Lys Met Lys Cys Ser Arg His Lys	Val Cys Ile Ala Gln Asp	
95	100	105
Ser Gln Thr Ala Val Cys Ile Ser His	Arg Arg Leu Thr His Arg	
110	115	120
Met Lys Glu Ala Gly Val Asp His Arg	Gln Trp Arg Gly Pro Ile	
125	130	135
Leu Ser Thr Cys Lys Gln Cys Pro Val	Val Tyr Pro Ser Pro Val	
140	145	150
Cys Gly Ser Asp Gly His Thr Tyr Ser	Phe Gln Cys Lys Leu Glu	
155	160	165
Tyr Gln Ala Cys Val Leu Gly Lys Gln	Ile Ser Val Lys Cys Glu	
170	175	180
Gly His Cys Pro Cys Pro Ser Asp Lys	Pro Thr Ser Thr Ser Arg	
185	190	195
Asn Val Lys Arg Ala Cys Ser Asp Leu	Glu Phe Arg Glu Val Ala	
200	205	210
Asn Arg Leu Arg Asp Trp Phe Lys Ala	Leu His Glu Ser Gly Ser	
215	220	225
Gln Asn Lys Lys Thr Lys Thr Leu Leu	Arg Pro Glu Arg Ser Arg	
230	235	240
Phe Asp Thr Ser Ile Leu Pro Ile Cys	Lys Asp Ser Leu Gly Trp	
245	250	255
Met Phe Asn Arg Leu Asp Thr Asn Tyr	Asp Leu Leu Leu Asp Gln	
260	265	270
Ser Glu Leu Arg Ser Ile Tyr Leu Asp	Lys Asn Glu Gln Cys Thr	
275	280	285
Lys Ala Phe Phe Asn Ser Cys Asp Thr	Tyr Lys Asp Ser Leu Ile	
290	295	300
Ser Asn Asn Glu Trp Cys Tyr Cys Phe	Gln Arg Gln Gln Asp Pro	
305	310	315
Pro Cys Gln Thr Glu Leu Ser Asn Ile	Gln Lys Arg Gln Gly Val	
320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345



Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
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Ile

<210> 443  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 443  
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<210> 444  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 444  
 catcatggtc atcaccacca tcatcatc 28

<210> 445  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 445  
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<210> 446  
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 <213> Homo sapiens

<400> 446

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 taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150  
 gaaacataga ctccaagtt ttaaacacct aaatgtgaat aacctatata 2200  
 tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250  
 tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300  
 tatgccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350  
 cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
 cttgatgagc aataatgata accagagagt gatttcattt aactcatag 2450  
 tagtataaaa agagatacat ttccctotta ggcccctggg agaagagcag 2500  
 cttagatttc cctactggca aggtttttta aaatgaggta aatgcogtat 2550  
 atgatcaatt accttaattg gccaagaaaa tgcttcaggt gtctaggggt 2600  
 atcctctgca aacttgcag acaaaggtc aataagatcc ttgcctatga 2650  
 ataccctcc cttttgcgct gttaaatttg caatgagaag caaatttaca 2700  
 gtaccataac taataaagca gggtagagat ataaactact gcatcttttc 2750  
 tataaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800  
 ctgtactctc tgactcctta cctaacaatg aatttgttac ataactttct 2850  
 acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900

taccatataa aaacgataat tgctttatth ggaaaagaat ttaggaatac 2950  
 taaggacaat tatttttata gacaaagtaa aaagacagat atttaagagg 3000  
 cataacaaaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatth 3050  
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100  
 tccattttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150  
 aacagctcat tttgtctttt tcaatataca aattttaaaa atactacaat 3200  
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250  
 cctcacacta aggctagag tttgctctga tatgcatttg gatgattaat 3300  
 gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350  
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 gtgaaattht aaaagacatt gattccgcat gtaaggatth ttcacttgaa 3500  
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550  
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600  
 aaattatcaa aggaaaa 3617

<210> 447  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 447  
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala  
 1 5 10 15  
 Ala Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro  
 20 25 30  
 Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys  
 35 40 45  
 Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile  
 50 55 60  
 Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His  
 65 70 75  
 Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys  
 80 85 90  
 Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met  
 95 100 105  
 Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile

110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu	
125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp	
140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser	
155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe	
170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val	
185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val	Val Met Val Val Val Ser	
200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg	
215	220	225
Lys Ser Arg Thr		

<210> 448  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
 cccagcaggg ctgggcgaca aga 23

<210> 449  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
 gtcttccagt ttcatatcca ata 23

<210> 450  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 450  
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<210> 451  
 <211> 859  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
 ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50  
 agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100  
 gccctgcccga gtgtgtcctg gatgctgctt tcctgcctca ttctcctgtg 150  
 tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200  
 gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250  
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
 ctctggaaaa ctgggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350  
 cctccctggg gaggagcatt agtaacagct actcatacat ctggattggg 400  
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550  
 ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600  
 gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650  
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700  
 ttctcccaa actgccctac ctgactacct tgtcatgatc ctcttctttt 750  
 ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800  
 gagatctcag agaataataa taaaaatggt actttataaa aaaaaaaaaa 850  
 aaaaaaaaaa 859

<210> 452  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 452  
 Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
   1                  5                  10                  15  
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
                   20                  25                  30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
                   35                  40                  45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50	55	60
Trp Met Asp Ala	Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys		
	65	70	75
Leu Val Ser Val	Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser		
	80	85	90
Leu Val Arg Ser	Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly		
	95	100	105
Leu His Asp Pro	Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp		
	110	115	120
Glu Trp Ser Ser	Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys		
	125	130	135
Asn Pro Ser Thr	Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser		
	140	145	150
Arg Ser Thr Gly	Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala		
	155	160	165
Lys Leu Pro Tyr	Val Cys Lys Phe Lys Asp		
	170	175	

<210> 453  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 453  
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 tgggggtgaga gcacagagga gtgggcccgg accatgcggg ggacgcggct 100  
 ggcgtcctctg ggcgtggtgc tggctgcctg cggagagctg gcgccggccc 150  
 tgcgtgtcta cgtctgtccg gagccacacag gagggtcgga ctgtgtcacc 200  
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
 ccgggagata gtgtaccctc tccaggggga ctccacgggtg accaagtcct 300  
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400  
 tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450  
 tccgactgta gaggccccgc ccacccccat ggccctatgc ggcccagccc 500  
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaaa aaaaaaaaaa 550

<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120

Leu Ser Leu Arg Leu  
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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gcgcagcggg agctaccggt gtctttgtcg cgatggtagc ggcggtcttc 200

ggcgggccacc ctctgctggg agtgagcgcc acctgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

accagggctc tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400

cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450

acgcagggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600



ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650  
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750  
 tctgggtccaa gatctgtaaa cctgtcctga aagaaggtca agtgtgtacc 800  
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900  
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950  
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
 gcattccaat aacaccttcc aaaaacctgg agtgaagag ctttgtttct 1100  
 ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattctca 1150  
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
 ggtgctgcac tgcctatttt tcctcttggt atgtaaattt ttgtacacat 1250  
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300  
 tttcagctta tagttcttaa aagcataacc ctttacccca tttaattcta 1350  
 gagtctagaa cgcaaggatc tcttggaaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala  
 1 5 10 15  
 Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
 20 25 30  
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75

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Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457  
 <211> 638  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
 509, 556  
 <223> unknown base

<400> 457  
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 ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggt 100  
 catttttttt tctttctcct tcnngagtc tnttgagang atggtttttg 150  
 gcgcagcggg agctaaccgc gttttttgtn gcgatggtag cggcgggttt 200

cggcggccac cttntgctgg gagtgcgc caccttgaat cggttttcaa 250  
 ttccaacgnt atcaagaacc tgccccacc gntgggcggc gctgcggggc 300  
 acccaggntt tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400  
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
 angcgggcgt gcaaantgt ntngcctgca ggaagcgccg aaaacgctgc 500  
 atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
 tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaacatca 600  
 ctgaaagctt tggaatgat catagcacct tggatggg 638

<210> 458  
 <211> 4040  
 <212> DNA  
 <213> Homo sapiens

<400> 458  
 gaggaaccta ccggtaccgg ccgcgcgctg gtagtcgccg gtgtggctgc 50  
 acctaccaa tcccgtgcgc cgcggctggg ccgtcggaga gtgcgtgtgc 100  
 ttctctcctg cagcgggtgc ttgggctcgg ccaggcggg tccgccgcca 150  
 gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
 gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
 ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300  
 tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350  
 accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400  
 agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450  
 gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500  
 atcaggatTT ttacagttta cttggagtgt ccaaaactgc aagcagtaga 550  
 gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600  
 aaaccgaat aaccctaatg cacatggcga ttttttaaaa ataaatagag 650  
 catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700  
 ggagaaaagg gacttgagga taatcaaggg ggccagtatg aaagctggaa 750  
 ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800  
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tttgtaaatt tttactcccc aggctgttca cactgccatg atttagctcc 900  
 cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950  
 ctgttaactg tggatgatgat agaatgcttt gccgaatgaa aggagtcaac 1000  
 agctatccca gtctcttcat ttttcggctc ggaatggccc cagtgaata 1050  
 tcatggagac agatcaaagg agagttagt gagttttgca atgcagcatg 1100  
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 caaactgctt ttgtgtctgg tattggctgg ctgatcactt tttgttcaa 1200  
 aggaggagat tgtttgactt cacagacag actcaggctt agtggcatgt 1250  
 tgtttctcaa ctcatggat gctaaagaaa tatatttga agtaatacat 1300  
 aatcttccag attttgaact actttcgga aacacactag aggatcgttt 1350  
 ggctcatcat cgggtggctgt tattttttca ttttgaaaa aatgaaaatt 1400  
 caaatgatcc tgagctgaaa aaactaaaa ctctacttaa aatgatcat 1450  
 attcaagttg gcaggtttga ctgttctct gcaccagaca tctgtagtaa 1500  
 tctgtatgtt tttcagccgt ctctagcagt atttaaagga caaggaacca 1550  
 aagaatatga aattcatcat ggaaagaaga ttctatatga tatacttgcc 1600  
 tttgcaaag aaagtgtgaa ttctcatgtt accacgcttg gacctcaaaa 1650  
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 ggtgtccacc atgtcgagct ttactaccag agttacgaag agcatcaa 1750  
 cttctttatg gtcagcttaa gtttggtaca ctagattgta cagtccatga 1800  
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 tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900  
 atcttgagat tcatagagga tcttatgaat ccttcagtgg tctcccttac 1950  
 acccaccacc ttcaacgaac tagttacaca aagaaaacac aacgaagtct 2000  
 ggatgggtga tttctattct ccgtggtgtc atccttgcca agtcttaatg 2050  
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 cagtatcaca gttacaatgg ttggaatagg gatgcttatt ccctgagaat 2250  
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tggaaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
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agaagggctc gcaaactttt tctgtaaagg gccggtttat aaatatatta 2850  
gactttgcag gctataatat atggttcaca catgagaaca agaataagagt 2900  
catcatgtat tctttgttat ttgcttttaa caacctttaa aaaatattaa 2950  
aacgattcct agctcagagc catacaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatgtt tcaggtggct 3050  
ggcttgaaca tgagtctgct gtgctatcta cataaatgtc taagttgtat 3100  
aaagtccact ttcccttcac gttttttggc tgacctgaaa agaggtaact 3150  
tagtttttgg tcaactgttc tcctaaaaat gctatcccta accatatatt 3200  
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ttatgctgta ttattatgag gagattcttc attgttttct ttccttctca 3300  
aaggttgaaa aaatgctttt aatttttcac agccgagaaa cagtgcagca 3350  
gtatatgtgc acacagtaag tacacaaatt tgagcaacag taagtcacac 3400  
aattctgtag tttgctgtat catccaggaa aacctgaggg aaaaaaatta 3450  
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ctttcataga aattttccca ctgatagttg atttttgagg catctaatat 3600  
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aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800  
 ttttcagata aatattgaca taataactga agttatTTTT ataagaaaat 3850  
 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900  
 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950  
 cagagtgtac agaattgtaa aaattccaat cagtcaaaag aggtcaatga 4000  
 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459  
 <211> 747  
 <212> PRT  
 <213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys	1	5	10	15
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val	20	25	30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				

	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser	Leu
	215	220	225
Val Ser Phe Ala	Met Gln His Val Arg	Ser Thr Val Thr Glu	Leu
	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala
	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys
	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu
	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn
	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg
	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn
	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu
	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala
	350	355	360
Pro Asp Ile Cys	Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu	Ala
	365	370	375
Val Phe Lys Gly	Gln Gly Thr Lys Glu	Tyr Glu Ile His His	Gly
	380	385	390
Lys Lys Ile Leu	Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser	Val
	395	400	405
Asn Ser His Val	Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala	Asn
	410	415	420
Asp Lys Glu Pro	Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys	Pro
	425	430	435
Pro Cys Arg Ala	Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn	Leu
	440	445	450
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val	His
	455	460	465
Glu Gly Leu Cys	Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr	Thr
	470	475	480
Val Val Phe Asn	Gln Ser Asn Ile His	Glu Tyr Glu Gly His	His
	485	490	495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro
				500					505					510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr
				515					520					525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro
				530					535					540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met
				545					550					555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys
				560					565					570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr
				575					580					585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln
				590					595					600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg
				605					610					615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr
				620					625					630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp
				635					640					645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
				725					730					735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
				740					745					

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 460  
actccccagg ctgttcacac tgcc 24

<210> 461  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
gatcagccag ccaataccag cagc 24

<210> 462  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

<400> 463  
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ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100  
caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcg ggtggaggaa actgcagctg 300  
agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgata 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt ttggtatcac aaaagcactt cttccatcga tgatggagag 550  
aaatcatggc cacatcgta cagtggcttc agtgtgcggc cacgaaggga 600  
ttccttacct catccatat tgttccagca aatttgccgc tgttggcttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

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aacctcatgt ctctgccag tttttgtgaa tactgggttc accaaaaatc 750  
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 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850  
 tatcaatatc tttctgagac tacagaagtt ttttcctgaa cgcgcctcag 900  
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 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150  
 gtagtttttc ataggtctgt ttttccttcc atgcctctta aaaacttctg 1200  
 tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250  
 catttaaagg tggacaaaag ctacctccct aaaagtaaata acaaagagaa 1300  
 cttattttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350  
 tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450  
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500  
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550  
 aactctgaag tccaccaaaa gtggaccctc tatatttcct ccctttttat 1600  
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 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700  
 ttcatatata cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
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 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
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 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
				35					40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185					190					195	
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
				290					295					300	

<210> 465  
 <211> 1547  
 <212> DNA  
 <213> Homo sapiens

<400> 465

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gctgtggctg gtgctggggg cggtgttcat gatcctgctg atcatcgtgt 200  
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aggccgcaca cggggccgcc gctgcccacg cccgggccgg acagggacag 300  
ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350  
gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400  
cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450  
gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcggg 500  
ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550  
aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650  
gcaccaactg gaagcgcggtg atgatcgtgc tgagcggaag cctgctgcac 700  
cgcggtgcgc cctaccgca cccgctgcgc atccgcgcg agcacgtgca 750  
caacgccagc gcgcacctga ccttcaacaa gttctggcgc cgctacggga 800  
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850  
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tgcggtgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000  
ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050  
ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
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ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200  
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gctgggagga ggactggttc gccaagatcc ccctggcctg gaggcagcag 1300  
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cgaaaacctc ctccgagact gaaagcttgc gcgttgcttt ttctcgcgtg 1400  
cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatttt 1450

gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500

atcgatattg tttttaaga ttaatatatt tcaggatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser	
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly	
				20					25					30	
Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr	
				35					40					45	
Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu	
				50					55					60	
Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser	
				65					70					75	
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln	
				80					85					90	
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp	
				95					100					105	
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln	
				110					115					120	
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser	
				125					130					135	
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro	
				140					145					150	
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala	
				155					160					165	
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg	
				170					175					180	
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro	
				185					190					195	
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala	
				200					205					210	
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys	
				215					220					225	
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys	
				230					235					240	

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
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 acgggatggc tacgggaacg cgctatgccg ggaagggtggg ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
 cggggcccca gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gtcacctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttgccg 350  
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450  
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 tcaaggggaat gtcataca tctccagcct ggtgggggca atcgccagag 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagcttttg cccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgtgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggctggg gctgcggcag tgttcctggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900  
 cccgatatac cttcctgatt tctctcattt ctacttgggg cccccttct 950  
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaac 1000  
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcaggttc 1050  
 ccataaaaac gatttgacg c 1071

<210> 468  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 468  
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 Asn Ser Gly Ala Arg Val Val Ile Cys Asp Lys Asp Glu Ser Gly  
 35 40 45  
 Gly Arg Ala Leu Glu Gln Glu Leu Pro Gly Ala Val Phe Ile Leu  
 50 55 60  
 Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu  
 65 70 75  
 Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala  
 80 85 90  
 Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln  
 95 100 105  
 Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr  
 110 115 120

09978299-101504

Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
				185					190					195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
				230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
				245					250					255	
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	
				260					265					270	

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
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 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgagggtca 300  
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgctg ccgcgcctc 500  
 tgcccgcac cgcgccgcac agggccttgc cgccagcgcg cagtcatgga 550



gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600

gccaggccag cagcccagaga ccatactcct tgcacctttg tgccaagaaa 650

ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470

<211> 180

<212> PRT

<213> Homo sapiens

<400> 470

Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
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Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
50 55 60

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
80 85 90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
95 100 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
110 115 120

Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
125 130 135

Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
140 145 150

Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
155 160 165

Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
170 175 180

<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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aaacccggcg ggcgagcgag gctgcggggc ggccgctgcc cttccccaca 100

09978299-101501

ctccccgccc agaagcctcg ctggcgccc aacatggcgg gtgggcgctg 150  
 cggccccgag ctaacggcgc tctggccgc ctggatcgcg gctgtggcgg 200  
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300  
 gctgaaatct tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggcgcgt tctttgtcac 450  
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatt 500  
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 caagaatata caccaaaaca atatgtcagc ttcccttttg cctgcagttt 1250  
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 gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
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 gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000  
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050  
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100  
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150  
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 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
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 agggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
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 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
			110						115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
			125						130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
			140						145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
			155						160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
			170						175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
			185						190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
			200						205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
			215						220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
			230						235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
			245						250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
			260						265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
			275						280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
			290						295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
			305						310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
			320						325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
			335						340					345

Asp Lys Gly Leu

<210> 473  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctcctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
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gcccatga tttgactcag agattctctt ttgtccacag acagtcatct 100  
caggggcaga aagaaaagag ctcccaaatg ctatatctat tcaggggctc 150  
tcaagaacaa tggaatatca tcttgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcatctc ctcttgggcg cctcattgct 300  
gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350  
gggtaccatg ggggttcttt ccagcccttg tcctcctaata tggattatat 400  
atgagaagag ctgttatcta ttcagcatgt cactaaatc ctgggatgga 450  
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500  
ctcaaataaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550  
attcattttg gataggcctt tctcggcccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650  
 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700  
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtca 850  
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 caagtagctg ggattacagt caggcaccac cacaccggc taattttgta 1850  
 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
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 gtagggaac tgctctcata ggaaagtgtt ctgcttttta aatacaaaaa 2050

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aaaaaaaaa aaaaaaaaaa aaaaaaaaa 2478

<210> 477  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

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Val Ile Tyr Asp	Gln Leu Cys Ser Val	Pro Ser Tyr Ser Ile Cys			
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Glu Lys Lys Phe	Ser Met				
	200				

<210> 478  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 478  
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<210> 479  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 479  
 acaagtgtct tcccaacctg 20

<210> 480  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 480  
 atcctcccag agccatggta cctc 24

<210> 481  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 481  
 ccaaggatag ctgttggttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482  
 <211> 3819  
 <212> DNA  
 <213> Homo sapiens



<400> 482

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 tcttggtcga tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150  
 tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgaact 200  
 ccgtcggagg aaaatgactc cccagtcgct gctgcagacg aactggttcc 250  
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 gaagactttc gcttctgcag ccagcggaac cagacacaca ggagcagcct 350  
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<210> 483  
 <211> 693  
 <212> PRT  
 <213> Homo sapiens

<400> 483  
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 Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu  
 20 25 30  
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

365	370	375
Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val	
380	385	390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu	
395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val	
410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg	
425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu	
440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro	
455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile	
470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu	
485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr	
500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly	
515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp	
530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly	
545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser	
560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn	
575	580	585
Met Ala Met Leu Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg	
590	595	600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu	
605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe	
620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile	
635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser	
650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

<400> 484  
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ctgctgctgg ccgtcttcct gctggacacg agcttcctgc tcagcgnagc 150  
cggaggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
cctgcacttc tcctgctcac ctgcctttcc tggatggggc tcgaggggta 250  
caacctctac cgactcgtgg tggaggtctt tggcacctat gtccttggt 300  
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400  
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450  
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500  
tttctgttca acatgg 516

<210> 485  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 485  
ggcattggag cagtgtggg tg 22

<210> 486  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgaggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

<400> 487  
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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200  
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250  
ccgccgtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300  
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cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
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099899-101501

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<210> 488  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 488  
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 20 25 30  
 Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln  
 35 40 45  
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser  
 50 55 60  
 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
 65 70 75  
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
 80 85 90  
 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
 95 100 105  
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
 110 115 120  
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
 125 130 135  
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
 140 145 150  
 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
 155 160 165  
 Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala  
 170 175 180  
 Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr  
 185 190 195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	200	205	210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	215	220	225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	230	235	240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	245	250	255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	260	265	270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	275	280	285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	290	295	300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	305	310	315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	320	325	330
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	335	340	345

<210> 489  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 489  
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<210> 490  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 490  
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<210> 491  
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 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491  
caccacagcg tttaaccagg 20

<210> 492  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 492  
acaacaggca cagttccac 20

<210> 493  
<211> 21  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 493  
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<210> 494  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 494  
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<210> 495  
<211> 3283  
<212> DNA  
<213> Homo sapiens

<400> 495  
cccattctcaa gctgatcttg gcacctctca tgctctgctc ttttcaacca 50  
gacctctaca ttccattttg gaagaagact aaaaatggtg tttccaatgt 100  
ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150  
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200  
tctggatggt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250  
tgacagaaat tcttgagggt attcccacga acaccacgaa cctcaccctc 300  
accattaacc acataccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400  
 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450  
 tttagtggac tcaacttattt aaaatccctt tacctggatg gaaaccagct 500  
 actagagata ccgcagggcc tccgcctag cttacagctt ctcagccttg 550  
 aggccaacaa catcttttcc atcagaaaag agaactctaac agaactggcc 600  
 aacatagaaa tactctacct gggccaaaac tgttattatc gaaatccttg 650  
 ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700  
 taaaagtgct ctccctgaaa gataacaatg tcacagccgt ccctactgtt 750  
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 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850  
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 ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200  
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acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496  
<211> 1049  
<212> PRT  
<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu	
1				5					10					15	
Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	
				20					25					30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	
				35					40					45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	
				50					55					60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	
				65					70					75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	
				80					85					90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	
				95					100					105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	
				110					115					120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	
				125					130					135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	
				140					145					150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	
				155					160					165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	
				170					175					180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	
				185					190					195	
Glu	Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser	
				200					205					210	
Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	
				215					220					225	
Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	
				230					235					240	
Gln	Glu	Asp	Asp	Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	
				245					250					255	

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Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480
Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp			

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu 560	Leu His Lys Leu Glu Val 565	
Leu Asp Ile Ser Ser Asn Ser His Tyr 575	Phe Gln Ser Glu Gly Ile 580	585
Thr His Met Leu Asn Phe Thr Lys Asn 590	Leu Lys Val Leu Gln Lys 595	600
Leu Met Met Asn Asp Asn Asp Ile Ser 605	Ser Ser Thr Ser Arg Thr 610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu 620	Glu Phe Arg Gly Asn His 625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp 635	Asn Arg Tyr Leu Gln Leu 640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu 650	Leu Asp Ile Ser Lys Asn 655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val 665	Phe Asp Gly Met Pro Pro 670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys 680	Asn Gly Leu Lys Ser Phe 685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys 695	Asn Leu Glu Thr Leu Asp 700	705
Leu Ser His Asn Gln Leu Thr Thr Val 710	Pro Glu Arg Leu Ser Asn 715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile 725	Leu Lys Asn Asn Gln Ile 730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln 740	Asp Ala Phe Gln Leu Arg 745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile 755	Gln Met Ile Gln Lys Thr 760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn 770	Leu Lys Met Leu Leu Leu 775	780
His His Asn Arg Phe Leu Cys Thr Cys 785	Asp Ala Val Trp Phe Val 790	795
Trp Trp Val Asn His Thr Glu Val Thr 800	Ile Pro Tyr Leu Ala Thr 805	810
Asp Val Thr Cys Val Gly Pro Gly Ala 815	His Lys Gly Gln Ser Val 820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu 830	Leu Asp Leu Thr Asn Leu 835	840



Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val  
 845 850 855  
 Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile  
 860 865 870  
 Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile  
 875 880 885  
 Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
 890 895 900  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys  
 905 910 915  
 Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu  
 920 925 930  
 Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln  
 935 940 945  
 Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys  
 950 955 960  
 Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His  
 965 970 975  
 Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe  
 980 985 990  
 Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys  
 995 1000 1005  
 Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln  
 1010 1015 1020  
 Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr  
 1025 1030 1035  
 Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val  
 1040 1045

<210> 497  
 <211> 4199  
 <212> DNA  
 <213> Homo sapiens

<400> 497  
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 cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150  
 gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200  
 tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250

gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300  
 catttcaagg gctgcaaaat ctactaaaa taaatctaaa ccacaacccc 350  
 aatgtacagc accagaacgg aaatcccggt atacaatcaa atggcttgaa 400  
 tatcacagac ggggcattcc tcaacctaaa aaacctagg gagttactgc 450  
 ttgaagacaa ccagttaccc caaataacct ctggtttgcc agagtctttg 500  
 acagaactta gtctaattca aaacaatata tacaacataa ctaaagaggg 550  
 catttcaaga cttataaact tgaaaaatct ctatttgcc tggaactgct 600  
 attttaacaa agtttgcgag aaaactaaca tagaagatgg agtatttgaa 650  
 acgctgacaa atttgaggtt gctatcacta tctttcaatt ctctttcaca 700  
 cgtgccaccc aaactgccaa gctccctacg caaacttttt ctgagcaaca 750  
 ccagatcaa atacattagt gaagaagatt tcaagggtt gataaattta 800  
 acattactag atttaagcgg gaactgtccg aggtgcttca atgccccatt 850  
 tccatgcgtg ccttgtgatg gtggtgcttc aattaatata gatcgttttg 900  
 cttttcaaaa cttgacccaa cttcgatacc taaacctctc tagcacttcc 950  
 ctcaggaaga ttaatgctgc ctggtttaaa aatatgcctc atctgaagg 1000  
 gctggatctt gaattcaact atttagtggg agaaatagtc tctggggcat 1050  
 ttttaacgat gctgccccgc ttagaaatac ttgacttgct ttttaactat 1100  
 ataaagggga gttatccaca gcatattaat atttccagaa acttctctaa 1150  
 acttttgtct ctacgggcat tgcatttaag aggttatgtg ttccaggaa 1200  
 tcagagaaga tgatttccag cccctgatgc agcttccaaa cttatcgact 1250  
 atcaacttgg gtattaattt tattaagcaa atcgatttca aacttttcca 1300  
 aaatttctcc aatctggaaa ttatttactt gtcagaaaac agaatatcac 1350  
 cgttggtaaa agatacccg cagagttatg caaatagtct ctcttttcaa 1400  
 cgtcatatcc ggaaacgacg ctcaacagat tttgagtttg acccacattc 1450  
 gaacttttat catttcccc gtcttttaat aaagccacaa tgtgctgctt 1500  
 atggaaaagc cttagattta agcctcaaca gtattttctt cattgggcca 1550  
 aaccaatttg aaaatcttcc tgacattgcc tgtttaaatc tgtctgcaaa 1600  
 tagcaatgct caagtgttaa gtggaactga attttcagcc attcctcatg 1650  
 tcaaatattt ggatttgaca aacaatagac tagactttga taatgctagt 1700

gctcttactg aattgtccga cttggaagtt ctagatctca gctataattc 1750  
acactatttc agaatagcag gcgtaacaca tcatctagaa tttattcaaa 1800  
atttcacaaa tctaaaagtt ttaaacttga gccacaacaa catttatact 1850  
ttaacagata agtataacct ggaaagcaag tccctggtag aattagtttt 1900  
cagtggcaat cgccttgaca ttttgtggaa tgatgatgac aacaggtata 1950  
tctccatttt caaaggcttc aagaatctga cacgtctgga tttatccctt 2000  
aataggctga agcacatccc aaatgaagca ttccttaatt tgccagcgag 2050  
tctcactgaa ctacatataa atgataatat gttaaagttt tttaactgga 2100  
cattactcca gcagtttccct cgtctcgagt tgcttgactt acgtggaaac 2150  
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gacactgctg ctgagtcata acaggatttc ccacctaccc tctggctttc 2250  
tttctgaagt cagtagtctg aagcacctcg atttaagttc caatctgcta 2300  
aaaacaatca acaaatccgc acttgaaaact aagaccacca ccaaattatc 2350  
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gtagatgtca tttgtgccag tcctggggat caaagaggga agagtattgt 2500  
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gcaaactctg agaaatgtgg tcttgactga aaatgattca cggataaca 3150

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 ttccgcgccat aataaagatg caaaggaatg acatttctgt attagttatc 3250  
 tattgctatg taacaaatta tcccaaaact tagtggttta aaacaacaca 3300  
 tttgctggcc cacagttttt gagggtcagg agtccaggcc cagcataact 3350  
 gggtcctctg ctccagggtgt ctccagggt gcaatgtagg tgttcaccag 3400  
 agacataggc atcactgggg tcacactcat gtggttggtt tctggattca 3450  
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 caccagctcc atgggagtga ccacctcagt ccagggaata cagctgaaga 3700  
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 ctgtaacatt tgacttctaa ggttttagatg ccatttaaga actgagatgg 4050  
 atagctttta aagcatcttt tacttcttac cattttttta aagtatgcag 4100  
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

Met	Glu	Asn	Met	Phe	Leu	Gln	Ser	Ser	Met	Leu	Thr	Cys	Ile	Phe
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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75
Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90
Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105
Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120
Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135
Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150
Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165
Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180
Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195
Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225
Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly
				245					250					255
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys
				260					265					270
Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn
				275					280					285
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg
				290					295					300
Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val
				305					310					315
Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly
				320					325					330
Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
				335					340					345

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Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	350	355	360
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	365	370	375
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	410	415	420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	455	460	465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	470	475	480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	485	490	495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	500	505	510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
Tyr	Ile	Ser	Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp			

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635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu	650	655
655	660	665
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met	665	670
670	675	680
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu	680	685
685	690	695
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp	695	700
700	705	710
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser	710	715
715	720	725
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val	725	730
730	735	740
Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr	740	745
745	750	755
Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser	755	760
760	765	770
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile	770	775
775	780	785
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile	785	790
790	795	800
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg	800	805
805	810	815
Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820
820	825	830
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835
835	840	845
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850
850	855	860
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865
865	870	875
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880
880	885	890
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895
895	900	905
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910
910	915	920
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925
925	930	

Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val
				935					940					945
Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe
				950					955					960
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile
				965					970					975
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu
				980					985					990
Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro
				995					1000					1005
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn
				1010					1015					1020
Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val
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Asp	Ser	Ile	Lys	Gln	Tyr									
				1040										

<210> 499  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 499  
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<210> 500  
 <211> 20  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 500  
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<210> 501  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 501  
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<210> 502



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Pressure	1.0	atm
Flow rate	1.0	L/min
Sample size	1.0	g
Time	1.0	min
Concentration	1.0	g/L
Volume	1.0	L
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>
Mass	1.0	g
Length	1.0	cm
Width	1.0	cm
Height	1.0	cm
Area	1.0	cm <sup>2</sup>
Volume	1.0	cm <sup>3</sup>

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<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 506  
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Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
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Lys Asp Ser

<210> 507  
<211> 1700  
<212> DNA  
<213> Homo sapiens

<400> 507

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gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
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<210> 508  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45  
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150  
 Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
 155 160 165  
 Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
 170 175 180  
 Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
 185 190 195  
 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
 200 205 210

09978299-101501

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
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Lys Asp Ser

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 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

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 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200  
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 ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 510  
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 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
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 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

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Arg Cys Val Asn Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp	Glu
155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly
170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala
185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu
200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala
215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu
230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu
245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys
260	265	270
Lys Asp Ser		

<210> 511  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 512  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 513  
 <211> 46  
 <212> DNA  
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<220>  
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<210> 514  
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<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

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atggccgcgt catgatggcc cgcaaaaagg gcattttcta cctgaccctt 500  
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cccagtgtgc tggatcgaag gggatattttg cactggagg aaagtggaag 1300  
tcgacctccc agtactcaag agaccagtag cagcctcttg ccacagagcc 1350  
cagccccac agaacacctg aactcaaag agatgccga ggacagcagc 1400  
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caggaatggc agtaataaaa gtctgcactt tggtcatttc tttcctcag 2150  
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gctaaccagt tcttcatta agcctcggct gactgaggga aagcccagca 2350  
ctgtgcctct ctcgggtaac tcacctaaag gcctcggccc acctctggct 2400  
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caccggcaga gtccagagc cacttcaccc tgggggtggg ctgtggcccc 2500  
cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550

attatatgtg gctatatttc ctagagcacc tgtgttttcc tctttctaag 2600  
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<210> 515  
<211> 364  
<212> PRT  
<213> Homo sapiens

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Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile  
35 40 45  
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu  
50 55 60  
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu  
65 70 75  
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp  
80 85 90  
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile  
95 100 105  
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln  
110 115 120  
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile  
125 130 135  
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro  
140 145 150  
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe  
155 160 165  
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn  
170 175 180  
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr  
185 190 195  
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser  
200 205 210  
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr  
215 220 225  
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

09978399-101501

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360
Glu Ala Glu Lys		

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 tttggctttg gactctcnet ttctcccaca gagcncttcg accatcactg 150  
 cccctgggtg ggggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcatcct tntctctccc cncctcaciaa tctatgtcct cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gccc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttggtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150  
 aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200  
 tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250  
 aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
 gtgcactatt gacaaccggg tcaccgggtt ggcctggcta aaccgcagca 350  
 ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400  
 cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450  
 tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
 caaagacctc taggggccac ctcatgtgc aagtatctcc caaattgta 550  
 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
 ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650  
 ctcccaaagc ggttggcttt gtgagtgaag acgaatactt ggaaattcag 700  
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 aactgcagtg gtgaagcctc agcagtcctc tcagcagaat tccagtggta 900  
 caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950  
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 gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250  
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300  
 gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagtttta 1350  
 aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400  
 cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450  
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aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
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 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523  
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 Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro  
 20 25 30  
 Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
 35 40 45  
 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
 50 55 60  
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
 65 70 75  
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
 80 85 90  
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
 95 100 105  
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
 110 115 120  
 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
 125 130 135  
 Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
 140 145 150  
 Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
 155 160 165  
 Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
 170 175 180  
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
 185 190 195  
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
 200 205 210  
 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
 215 220 225  
 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

09978299-10501

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524  
 <211> 503  
 <212> DNA  
 <213> Homo sapiens

<400> 524  
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 cgtgcgagc ggagatgcca ccttcccaa agctatggac aacgtgacgg 150  
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 gag 503

<210> 525  
 <211> 2602  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
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aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200  
agcaggtgcc tctctactgc tggctgcact gcttctgggc tgccttgtgg 250  
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 cctccagcag agccccacc attcactgtg acatctttcc gtgtcaccct 2550  
 gcctggaaga ggtctgggtg gggaggccag ttcccatagg aaggagtctg 2600  
 cc 2602

<210> 526  
 <211> 736  
 <212> PRT  
 <213> Homo sapiens

<400> 526  
 Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Val Gly  
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 Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu  
 20 25 30

Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu	35	40	45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro	50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly	65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu	140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro	155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly	170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser			

Glu Pro Val Val	Val Tyr Gly Met Asp	Tyr Leu Gln Gln Val	Ser
335		340	345
Glu Leu Ile Asn	Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr	Leu
350		355	360
Ile Trp Asn Leu	Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg	Arg
365		370	375
Phe Glu Ser Ala	Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly	Thr
380		385	390
Lys Lys Ser Cys	Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn	Thr
395		400	405
Asp Asp Ala Leu	Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys	Ala
410		415	420
Thr Phe Asp Arg	Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile	Ser
425		430	435
Glu Ile Arg Thr	Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val	Trp
440		445	450
Met Asp Glu Lys	Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp	Ala
455		460	465
Ile Tyr Asp Met	Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro	Lys
470		475	480
Glu Leu Asp Asp	Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp	Ser
485		490	495
Phe Phe Gln Asn	Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys	Val
500		505	510
Met Ala Asp Gln	Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp	Ser
515		520	525
Met Thr Pro Gln	Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys	Asn
530		535	540
Glu Ile Val Phe	Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr	Ala
545		550	555
Arg Asn His Pro	Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val	Val
560		565	570
Met Gly His Glu	Leu Thr His Ala Phe	Asp Asp Gln Gly Arg	Glu
575		580	585
Tyr Asp Lys Glu	Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu	Ser
590		595	600
Leu Ala Ala Phe	Arg Asn His Thr Ala	Cys Met Glu Glu Gln	Tyr
605		610	615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr	620	625	630
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr	635	640	645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln	650	655	660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly	665	670	675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His	680	685	690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	695	700	705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	710	715	720
Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val	725	730	735

Trp

<210> 527  
 <211> 4308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1478, 3978, 4057-4058, 4070  
 <223> unknown base

<400> 527  
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 agcctcccg ccccgccggc cccgctgctg ctctcgggc tgctgctgct 150  
 cggctcccg cggccccgcg gcgcgggcc agagcccccc gtgctgcca 200  
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 gggcagcccc cggggcgga cacggcgga gctgggcagc ggcctccagc 450  
 caagcccgtc cccgcaggct gcaccttcgg cgggaaggtc tatgccttgg 500

105107 66282660

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200  
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 <211> 352  
 <212> PRT  
 <213> Homo Sapien

<400> 612

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				20					25					30
Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
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Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
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Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
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Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
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Pro	Pro	Lys	Ile	Tyr	Asp	Ile	Ser	Asn	Asp	Met	Thr	Val	Asn	Glu
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Gly	Thr	Asn	Val	Thr	Leu	Thr	Cys	Leu	Ala	Thr	Gly	Lys	Pro	Glu
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Pro	Ser	Ile	Ser	Trp	Arg	His	Ile	Ser	Pro	Ser	Ala	Lys	Pro	Phe
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Glu	Asn	Gly	Gln	Tyr	Leu	Asp	Ile	Tyr	Gly	Ile	Thr	Arg	Asp	Gln
				185					190					195
Ala	Gly	Glu	Tyr	Glu	Cys	Ser	Ala	Glu	Asn	Ala	Val	Ser	Phe	Pro
				200					205					210
Asp	Val	Arg	Lys	Val	Lys	Val	Val	Val	Asn	Phe	Ala	Pro	Thr	Ile
				215					220					225
Gln	Glu	Ile	Lys	Ser	Gly	Thr	Val	Thr	Pro	Gly	Arg	Ser	Gly	Leu

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230	235	240
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245	250	255
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260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
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Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
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Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
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Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

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Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
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Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu	
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 35 40 45  
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
 50 55 60  
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
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agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100  
acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150  
caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200  
gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250  
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<210> 618  
<211> 750  
<212> PRT  
<213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala
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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
				35					40					45
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
				50					55					60
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
				65					70					75
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
				80					85					90

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Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser			

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380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu
395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser
410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala
425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile
440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp
455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu
470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu
485	490	495
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met Pro
500	505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe Phe
515	520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys Asn
530	535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser Val
545	550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met Phe
560	565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val Phe
575	580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp Tyr
590	595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile Ser
605	610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe Asp
620	625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser Lys
635	640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile Val
650	655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala Phe
665	670	675

Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val
				680					685					690
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe
				695					700					705
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp
				710					715					720
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala
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Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala
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cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50

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